

FIGURE 1

CGGACGCGTGGGTGCGAGGCGAAGGTGACCGGGGACCGAGCATTTTCAGATCTGCTCGGTAGA
CCTGGTGCACCACCACC**ATG**TTGGCTGCAAGGCTGGTGTGTCTCCGGACACTACCTTCTAGG
GTTTTCCACCCAGCTTTACCAAGGCCTCCCCTGTTGTGAAGAATTCCATCACGAAGAATCA
ATGGCTGTTAACACCTAGCAGGGAATATGCCACCAAAACAAGAATTGGGATCCGGCGTGGGA
GAACTGGCCAAGAACTCAAAGAGGCAGCATTTGGAACCATCGATGGAAAAAATATTTAAATTT
GATCAGATGGGAAGATGGTTTGTGCTGGAGGGGCTGCTGTTGGTCTTGGAGCATTGTGCTA
CTATGGCTTGGGACTGTCTAATGAGATTGGAGCTATTGAAAAGGCTGTAATTTGGCCTCAGT
ATGTCAAGGATAGAATTCATTCCACCTATATGTACTTAGCAGGGAGTATTGGTTTAAACAGCT
TTGTCTGCCATAGCAATCAGCAGAACGCCTGTTCTCATGAACCTTCATGATGAGAGGCTCTTG
GGTGACAATTGGTGTGACCTTTGCAGCCATGGTTGGAGCTGGAATGCTGGTACGATCAATAC
CATATGACCAGAGCCCAGGCCCAAAGCATCTTGCTTGGTTGCTACATTCTGGTGTGATGGGT
GCAGTGGTGGCTCCTCTGACAATATTAGGGGGTCTCTCTCATCAGAGCTGCATGGTACAC
AGCTGGCATTTGTGGGAGGCCTCTCCACTGTGGCCATGTGTGCGCCCAGTGAAAAGTTTCTGA
ACATGGGTGCACCCCTGGGAGTGGGCCTGGGTCTCGTCTTTGTGTCCTCATTGGGATCTATG
TTTCTTCCACCTACCACCGTGGCTGGTGCCACTCTTTACTCAGTGGCAATGTACGGTGGATT
AGTTCTTTTTCAGCATGTTTCTTCTGTATGATACCCAGAAAGTAATCAAGCGTGCAGAAGTAT
CACCAATGTATGGAGTTCAAAAATATGATCCCATTAACCTCGATGCTGAGTATCTACATGGAT
ACATTAAATATATTTATGCGAGTTGCAACTATGCTGGCAACTGGAGGCAACAGAAAGAA**AG**
AAGTGACTCAGCTTCTGGCTTCTCTGCTACATCAAATATCTTGTTTAAATGGGGCAGATATGC
ATTAAATAGTTTGTACAAGCAGCTTTCGTTGAAGTTTAGAAGATAAGAAACATGTCATCATA
TTTAAATGTTCCGGTAATGTGATGCCTCAGGTCTGCCTTTTTTTCTGGAGAATAAATGCAGT
AATCCTCTCCCAAATAAGCACACACATTTTCAATTCTCATGTTTGAGTGATTTTAAATGTT
TTGGTGAATGTGAAAATAAAGTTTGTGTGTCATGAGAATGTAAGTCTTTTTTCTACTTTAAAA
TTTAGTAGGTTCACTGAGTAACTAAAATTTAGCAAACCTGTGTTTGCATATTTTTTTGGAGT
GCAGAATATTGTAATTAATGTCATAAGTGATTTGGAGCTTTGGTAAAGGGACCAGAGAGAAG
GAGTCACCTGCAGTCTTTTGTTTTTTTAAATACTTAGAACTTAGCACTTGTGTTATTGATTA
GTGAGGAGCCAGTAAGAAACATCTGGGTATTTGGAACAAGTGGTCATTGTTACATTCATTT
GCTGAACCTAACAAAACCTGTTTCATCCTGAAACAGGCACAGGTGATGCATTCTCCTGCTGTTG
CTTCTCAGTGCTCTCTTTCCAATATAGATGTGGTCATGTTTGACTTGTACAGAATGTTAATC
ATACAGAGAATCCTTGATGGAATTATATATGTGTGTTTACTTTTGAATGTTACAAAAGGAA
ATAACTTTTAAACTATTTCTCAAGAGAAAATATTCAAAGCATGAAATATGTTGCTTTTTCCAG
AATACAAACAGTATACTCATG

CGGACGCGTGGGTGCGAGGCGAAGGTGACCGGGGACCGAGCATTTTCAGATCTGCTCGGTAGA

FIGURE 3

GAAGGCTGCCTCGCTGGTCCGAATTCCGGTGGCGCCACGTCCGCCCGTCTCCGCTTCTGCAT
 CGCGGCTTCGGCGGCTTCCACCTAGACACCTAACAGTCGCGGAGCCGGCCGCGTCTGAGGG
 GGTCCGCACGGGGAGTCGGGCGGTCTTGTCATCTTGCTACCTGTGGGTCTGAAG**ATGT**CGG
 ACATCGGAGACTGGTTTCAGGAGCATCCCGGCGATCACGCGCTATTGGTTCCGCCACCGTC
 GCCGTGCCCTTGGTCGGCAAACCTCGGCCTCATCAGCCCGGCCTACCTCTTCCCTCTGGCCCGA
 AGCCTTCCCTTATCGCTTTCAGATTTGGAGGCCAATCACTGCCACCTTTTATTTCCCTGTGG
 GTCCAGGAACCTGGATTTCTTTATTTGGTCAATTTATATTTCTTATATCAGTATTCTACGCGA
 CTTGAAACAGGAGCTTTTGATGGGAGGCCAGCAGACTATTTATTCATGCTCCTCTTTAACTG
 GATTTGCATCGTGATTACTGGCTTAGCAATGGATATGCAGTTGCTGATGATTCCCTCTGATCA
 TGTCAGTACTTTATGTCTGGGCCCAGCTGAACAGAGACATGATTGTATCATTTTGGTTTGA
 ACACGATTTAAGGCCTGCTATTTACCCTGGGTTATCCTTGGATTCAACTATATCATCGGAGG
 CTCGGTAATCAATGAGCTTATTGGAAATCTGGTTGGACATCTTTATTTTCTTAATGTTCA
 GATACCCAATGGACTTGGGAGGAAGAAATTTCTATCCACACCTCAGTTTTTGTACCGCTGG
 CTGCCAGTAGGAGAGGAGGAGTATCAGGATTTGGTGTGCCCCCTGCTAGCATGAGGCGAGC
 TGCTGATCAGAATGGCGGAGGCGGGAGACACAACCTGGGGCCAGGGCTTTCGACTTGGAGACC
 AG**TGA**AGGGGGCGGCCTCGGGCAGCCGCTCCTCTCAAGCCACATTTCCCTCCAGTGCTGGGTG
 CACTTAACAACCTGCGTTCTGGCTAACACTGTTGGACCTGACCCACACTGAATGTAGTCTTTC
 AGTACGAGACAAAGTTTCTTAAATCCCGAAGAAAAATATAAGTGTTCCACAAGTTTCACGAT
 TCTCATTCAAGTCCTTACTGCTGTGAAGAACAATAACCAACTGTGCAAATTGCAAACTGAC
 TACATTTTTTGGTGTCTTCTCTTCTCCCTTTCCGTCTGAATAATGGGTTTTAGCGGGTCTT
 AATCTGCTGGCATTGAGCTGGGGCTGGGTACCAAAACCTTCCCAAAGGACCTTATCTCTT
 TCTTGACACATGCCTCTCTCCACTTTTCCCAACCCCCACATTTGCAACTAGAAAAAGTTG
 CCCATAAAATTGCTCTGCCCTTGACAGGTTCTGTTATTTATTGACTTTTGCCAAGGCTGGTC
 ACAACAATCATATTCACGTTATTTTCCCTTTTGGTGGCAGAACTGTTACCAATAGGGGGAG
 AAGACAGCCACGGATGAAGCGTTTCTCAGCTTTTGGAAATTGCTTCGACTGACATCCGTTGTT
 AACCGTTTGCCACTCTTCAGATATTTTTTATAAAAAAAGTACCAGTTCATGAGGGCCA
 CAGATTGGTTATTAATGAGATACGAGGGTTGGTGTGGTGTGTTTCTTCTGAGCTAAGTGA
 TCAAGACTGTAGTGGAGTTGCAGCTAACATGGGTTAGGTTTAAACCATGGGGGATGCACCCC
 TTTGCCGTTTCATATGTAGCCCTACTGGCTTTGTGTAGCTGGAGTAGTTGGGTTGCTTTGTGT
 TAGGAGGATCCAGATCATGTTGGCTACAGGGAGATGCTCTCTTTGAGAGGTCCTGGGCATTG
 ATTCCCATTTCAATCTCATTCTGGATATGTGTTTATTGAGTAAAGGAGGAGAGACCCTCATA
 CGCTATTTAAATGTCACTTTTTTGCCTATCCCCCGTTTTTTGGTCATGTTTCAATTAATTGT
 GAGGAAGGCGCAGCTCCTCTCTGCACGTAGATCATTTTTTAAAGCTAATGTAAGCACATCTA
 AGGGAATAACATGATTTAAGGTTGAAATGGCTTTAGAATCATTTGGGTTTGAGGGTGTGTTA
 TTTTGAGTCATGAATGTACAAGCTCTGTGAATCAGACCAGCTTAAATACCCACACCTTTTTT
 TCGTAGGTGGGCTTTTCCCTATCAGAGCTTGGCTCATAACCAAATAAAGTTTTTTGAAGGCCA
 TGGCTTTTTCACACAGTTATTTTATTTTATGACGTTATCTGAAAGCAGACTGTTAGGAGCAGT
 ATTGAGTGGCTGTACACTTTGAGGCAACTAAAAAGGCTTCAAACGTTTTGATCAGTTTCTT
 TTCAGGAAACATTGTGCTCTAACAGTATGACTATTCTTTCCCCACTCTTAAACAGTGTGAT
 GTGTGTTATCCTAGGAAATGAGAGTTGGCAAACAACCTTCTCATTTTGAATAGAGTTTGTGTG
 TACTTCTCCATATTTAATTTATATGATAAAATAGGTGGGGAGAGTCTGAACCTTAACTGTCA
 TGTTTTGTTGTTTCTGTGGCCACAATAAAGTTTACTTGTAAAATTTTAGAGGCCATTACT
 CCAATTATGTTGCACGTACACTCATTTGTACAGGCGTGGAGACTCATTGTATGTATAAGAATA
 TTTCTGACAGTGAGTGACCCGGAGTCTCTGGTGTACCCTCTTACCAGTCAGCTGCCTGCGAG
 CAGTCATTTTTTCCCTAAAGGTTTACAAGTATTTAGAAGTTTTTCAGTTCAGGGCAAATGTTT
 ATGAAGTTATTCCTCTTAAACATGGTTAGGAAGCTGATGACGTTATTGATTTTGTCTGGATT
 ATGTTTCTGGAATAATTTTACCAAAACAAGCTATTTGAGTTTTGACTTGACAAGGCAAAACA
 TGACAGTGGATTCTCTTTACAAATGGAAAAAATAATCCTTATTTTGTATAAAGGACTTCCC
 TTTTGTAACTAATCCTTTTTTATTGGTAAAAATTGTAAATTAAATGTGCAACTTG

FIGURE 4

MSDIGDWFRSIPAITRYWFAATVAVPLVGKLGKISPAYLFLWPEAFLYRFQIWRPITATFYF
PVGPGTGFLYLVLNLYFLYQYSTRLETGAFGDRPADYLFMLLFNWICIVITGLAMDMQLLMI
LIMSVLYVWAQLNRDMIVSFWFGTRFKACYLPWVILGFNYIIGGSVINELIGNLVGHLYFFL
MFRYPMDLGGRNFLSTPQFLYRWLPSRRGGVSGFGVPPASMRRAADQNGGGGRHNWGQGFR
LDQ

Transmembrane domain:

amino acids 98-116, 152-172

N-myristoylation site.

amino acids 89-95, 168-174, 176-182, 215-221, 221-227, 237-243

Glycosaminoglycan attachment site.

amino acids 218-222

FIGURE 5

GGGGCCGCGGTCTAGGGCGGCTACGTGTGTTGCCATAGCGACCATTTTGCATTAACTGGTTG
 GTAGCTTCTATCCTGGGGGCTGAGCGACTGCGGGCCAGCTCTTCCCCTACTCCCTCTCGGCT
 CCTTGTGGCCCAAAGGCCTAACCAGGGGTCCGGCGGTCTGGCCTAGGGATCTTCCCCGTTGCC
 CCTTTGGGGCGGG**ATG**GCTGCGGAAGAAGAAGACGAGGTGGAGTGGGTAGTGGAGAGCATCG
 CGGGGTTTCTGCGAGGCCCAGACTGGTCCATCCCCATCTTGGACTTTGTGGAACAGAAATGT
 GAAGTTAACTGCAAAGGAGGGCATGTGATAACTCCAGGAAGCCCAGAGCCGGTGATTTTGGT
 GGCCTGTGTTCCCCTTGTTTTTGTATGATGAAGAAGAAAGCAAATTGACCTATACAGAGATTC
 ATCAGGAATACAAAGAACTAGTTGAAAAGCTGTTAGAAGGTTACCTCAAAGAAATTGGAATT
 AATGAAGATCAATTTCAAGAAGCATGCACTTCTCCTCTTGCAAAGACCCATACATCACAGGC
 CATTTTGCACCTGTGTTGGCAGCAGAAGATTTTACTATCTTTAAAGCAATGATGGTCCAGA
 AAAACATTGAAATGCAGCTGCAAGCCATTCGAATAATTCAAGAGAGAAATGGTGTATTACCT
 GACTGCTTAACCGATGGCTCTGATGTGGTCAGTGACCTTGAACACGAAGAGATGAAAATCCT
 GAGGGAAGTTCTTAGAAAATCAAAAGAGGAATATGACCAGGAAGAAGAAAGGAAGAGGAAAA
 AACAGTTATCAGAGGCTAAAACAGAAGAGCCACAGTGCATTCCAGTGAAGCTGCAATAATG
 AATAATTCCCAAGGGGATGGTGAACATTTTGCACACCCACCCCTCAGAAGTTAAAATGCATTT
 TGCTAATCAGTCAATAGAACCTTTGGGAAGAAAAGTGGAAAGGTCTGAAACTTCCTCCCTCC
 CACAAAAGGCCTGAAGATTCCTGGCTTAGAGCATGCGAGCATTGAAGGACCAATAGCAAAC
 TTATCAGTACTTGAACAGAAGAAGCTTCGGCAACGAGAACACTATCTCAAGCAGAAGAGAGA
 TAAGTTGATGTCCATGAGAAAGGATATGAGGACTAAACAGATACAAAATATGGAGCAGAAAG
 GAAAACCCACTGGGGAGGTAGAGGAAATGACAGAGAAACCAGAAATGACAGCAGAGGAGAAG
 CAAACATTACTAAAGAGGAGATTGCTTGCAGAGAACTCAAAGAAGAAGTTATTAATAAG**TA**
ATAATTAAGAACAATTTAACAAAATGGAAGTTCAAATTGTCTTAAAAATAAATTATTTAGTC
 CTTACACTG

FIGURE 6

MAAEEDEVEWVESIAGFLRGPDWSIPILDFVEQKCEVNCKGGHVITPGSPEPVILVACVP
LVFDDEEESKLTYTEIHQEYKELVEKLLEGYLKEIGINEDQFQEAactsSPLAKTHTSQAILQP
VLAAEDFTIFKAMMVQKNIEMQLQAIRIIQERNGVLPDCLTDGSDVVSDLEHEEMKILREVL
RKSKEEYDQEEERKRKKQLSEAKTEEPTVHSSEAAIMNNSQGDGEHFAHPPSEVKMHFANQS
IEPLGRKVERSETSSLPQKGLKIPGLEHASIEGPIANLSVLGTEELRQREHYLKQKRDKLMS
MRKDMRTKQIQNMEQKGKPTGEVEEMTEKPEMTAEKQTLLKRRLLAEKLKEEVINK

N-glycosylation sites.

amino acids 224-228, 246-250, 285-289

N-myristoylation site.

amino acids 273-279

Amidation site.

amino acids 252-256

Cytosolic fatty-acid binding proteins.

amino acids 78-108

7/330

FIGURE 7

GGGCACAGCACATGTGAAGTTTTTGATGATGAAGAAGAAAGCAAATTGACCTATACAGAGAT
TCATCAGGAATACAAAGAACTAGTTGAAAAGCTGTTAGAAGGTTACCTCAAAGAAATTGGAA
TTAATGAAGATCAATTTCAAGAAGCATGCACTTCTCCTCTTGCAAAGACCCATACATCACAG
GCCATTTTTGCAACCTGTGTTGGCAGCAGAAGATTTTACTATCTTTAAAGCAATGATGGTCC
AGAAAAACATTGAAATGCAGCTGCAAGCCATTCTGAATAATTCAAGAGAGAAATGGTGTATTA
CCTGACTGCTTAACCGATGGCTCTGATGTGGTCAGTGACCTTGAACACGAAGAGATGAAAAT
CCTGAGGGAAGTTCTTAGAAAATCAAAAGAGGAATATGACCAGGAA

0994134-11694

FIGURE 8

CCGTGGTTTTTGTTCTGCAATAGCGGGCTTAGAGGAGGGGCTTTTTTCGCCTATACCTACTG
TAGCTTCTCCACGTATGGACCCCTAAAGGCTACTGCTGCTACTACGGGGCTAGACAGTTACTG
TCTCAGCTCTAGGATGTGCGTTCTTCCACTAGAAGCTCTTCTGAGGGAGGTAATTA AAAAAC
AGTGGA**ATG**GAAAAACAGTGCTGTAGTCATCCTGTAATATGCTCCTTGTCACCAATGTATAC
ATTCTGCTAGGTGCCATATTCATTGCTTTAAGCTCAAGTCGCATCTTACTAGTGAAGTATT
CTGCCAATGAAGAAAACAAGTATGATTATCTTCCAACACTGTGAATGTGTGCTCAGAACTG
GTGAAGCTAGTTTTCTGTGTGCTTGTGTATCTGTGTTATAAAGAAAGATCATCAAAGTAG
AAATTTGAAATATGCTTCCCTGGAAGGAATTCTCTGATTTTCATGAAGTGGTCCATTCCCTGCCT
TTCTTTATTTCCCTGGATAACTTGATTGTCTTCTATGTCTGTCTCTATCTTCAACCAGCCATG
GCTGTTATCTTCTCAAATTTTAGCATTATAACAACAGCTCTTCTATTTCAGGATAGTGCTGAA
GAGGCGTCTAAACTGGATCCAGTGGGCTTCCCTCCTGACTTTATTTTTTGTCTATTGTGGCCT
TGACTGCCGGGACTAAAACCTTTACAGCACAACTTGGCAGGACGTGGATTTTCATCACGATGCC
TTTTTCAGCCCTTCCAATTCCTGCCTTCTTTTCAGAAGTGAGTGTCCAGAAAAGACAATTG
TACAGCAAAGGAATGGACTTTTCTGAAGCTAAATGGAACACCACAGCCAGAGTTTTTCAGTC
ACATCCGTCTTGGCATGGGCCATGTTCTTATTATAGTCCAGTGTTTTATTTCTTCAATGGCT
AATATCTATAATGAAAAGATACTGAAGGAGGGGAACCAGCTCACTGAAAGCATCTTCATACA
GAACAGCAAACCTCTATTTCTTTGGCATTCTGTTAATGGGCTGACTCTGGGCCTTCAGAGGA
GTAACCGTGATCAGATTAAAGAACTGTGGATTTTTTTTATGGCCACAGTGCATTTTCAGTAGCC
CTTATTTTTTGTAACTGCATTCCAGGGCCTTTTCAGTGGCTTTTCATTCTGAAGTTCCTGGATAA
CATGTTCCATGTCTTGATGGCCCAGGTTACCACTGTCAATTATCACAAACAGTGTCTGTCTCTG
TCTTTGACTTTCAGGCCCTCCCTGGAATTTTTCTTGAAGCCCCATCAGTCCTTCTCTCTATA
TTTATTTTATAATGCCAGCAAGCCTCAAGTTCGGAATACGCACCTAGGCAAGAAAGGATCCG
AGATCTAAGTGGCAATCTTTGGGAGCGTTCAGTGGGGATGGAGAAGAACTAGAAAGACTTA
CCAAACCCAAGAGTGATGAGTCAGATGAAGATACTTTCT**TA**ACTGGTACCCACATAGTTTGCA
GCTCTCTTGAACCTTATTTTTCACATTTTTCAGTGTGTTGTAATATTTATCTTTTCACTTTGATA
AACCAGAAATGTTTCTAAATCCTAATATTCTTTGCATATATCTAGCTACTCCCTAAATGGTT
CCATCCAAGGCTTAGAGTACCCAAAGGCTAAGAAATTCTAAAGAACTGATACAGGAGTAACA
ATATGAAGAATTCAATTAATATCTCAGTACTTGATAAATCAGAAAGTTATATGTGCAGATTAT
TTTCCTTGGCCTTCAAGCTTCCAAAAAACTTGTAAATAATCATGTTAGCTATAGCTTGTATAT
ACACATAGAGATCAATTTGCCAAATATTCACAATCATGTAGTTCTAGTTTACATGCCAAAGT
CTTCCCTTTTTTAACATTATAAAAAGCTAGGTTGTCTCTTGAATTTTGAGGCCCTAGAGATAGT
CATTTTGCAAGTAAAGAGCAACGGGACCCTTTCTAAAAACGTTGGTTGAAGGACCTAAATAC
CTGGCCATACCATAGATTTGGGATGATGTAGTCTGTGCTAAATATTTTGCTGAAGAAGCAGT
TTCTCAGACACAACATCTCAGAATTTTAATTTTTTAGAAATTCATGGGAAATTGGATTTTTGT
AATAATCTTTTGATGTTTTAAACATTGGTTCCCTAGTCACCATAGTTACCACTTGTATTTTA
AGTCATTTAAACAAGCCACGGTGGGGCTTTTTTCTCCTCAGTTTGAGGAGAAAAATCTTGAT
GTCATTACTCCTGAATTATTACATTTTGGAGAATAAGAGGGCATTTTATTTTATTAGTTACT
AATTCAAGCTGTGACTATTGTATATCTTTCCAAGAGTTGAAATGCTGGCTTCAGAATCATAC
CAGATTGTGAGTGAAGCTGATGCCTAGGAACTTTTAAAGGGATCCTTTCAAAGGATCAGTT
AGCAAACACATGTTGACTTTTAACTGATGTATGAATATTAATACTCTAAAAATAGAAAGACC
AGTAATATATAAGTCACTTTACAGTGCTACTTCACACTTAAAAGTGCATGGTATTTTTTCATG
GTATTTTGCATGCAGCCAGTTAACTCTCGTAGATAGAGAAGTCAGGTGATAGATGATATTAA
AAATTAGCAAACAAAAGTGACTTGCTCAGGGTCATGCAGCTGGGTGATGATAGAAGAGTGGG
CTTTAACTGGCAGGCCTGTATGTTTACAGACTACCATACTGTAAATATGAGCTTTTATGGTGT
CATTCTCAGAACTTATACATTTCTGCTCTCCTTTCTCCTAAGTTTCATGCAGATGAATATA
AGGTAATATACTATTATATAATTCATTTGTGATATCCACAATAATATGACTGGCAAGAATTG
GTGGAAATTTGTAATTAAAATAATTATTAAACCT

FIGURE 9

MEKQCCSHPVICSLSTMYTFLLGAIFIALSSSRILLVKYSANEENKYDYLPTTVNVCSELVK
LVFCVLVSFCVIKKDHQSRNLKYASWKEFSDFMKWSIPAFLYFLDNLIVFYVLSYLQPAMAV
IFSNFSIITTALLFRIVLKRRLNWIQWASLLTLELSIVALTAGTKTLQHNLAGRGFHHDAFF
SPSNSCLLFRSECPRKDNCTAKEWTFPEAKWNTTARVFSHIRLGMGHVLIIVQCFISSMANI
YNEKILKEGNQLTESIFIQNSKLYFFGILFNGLTLGLQRSNRDQIKNCGFFYGHSAFSVALI
FVTAFAQGLSVAFILKFLDNMFHVLMAQVTTVIITTVSVLVDFRPSLEFFLEAPSVLLSIFI
YNASKPQVPEYAPRQERIRDLSGNLWERSSSGDGEELERLTKPKSDESDETF

Transmembrane domains:

amino acids 16-36 (type II), 50-74, 147-168, 229-250, 271-293,
298-318, 328-368

N-glycosylation sites.

amino acids 128-132, 204-208, 218-222, 374-378

Glycosaminoglycan attachment site.

amino acids 402-406

N-myristoylation sites.

amino acids 257-263, 275-281, 280-286, 284-290, 317-323

CGTGCCTGCGCAATGGGTGTCGGGTCCGCTTTTTCCCAATCCGGACGTAATCGTGGTTTTTTG
TTCTGCAATAGGCGGCTTAGAGGGAGGGGCTTTTTCGCCTATACCTACTGTAGCTTCTCCAC
GTATGGACCCTAAAGGCTACTGCTGCTACTACGGGGCTAGACAGTTACTGTCTCAGCTCTAG
GATGTGCGTTCTTCCACTAGAAGCTCTTCTGAGGGAGGTAATTAAAAACAGTGGAATGGA
AAACAGTGCTGTAGTCATCCTGTAATATGCTCCTTGTCAACAATGTATACATTCCTGCTAGG
TGCCATATTCATTGCTTTAAGCTCAAGTCGCATCTTACTAGTGAAGTATTCTGCCAATGAAG
AAAACAAGTATGATTATCTTCCAACACTACTGTGAATGTGTGCTCAGAACTGGTGAAGCTAGTT
TTCTGTGTGCTTGTGTCAATTCTGTGTTATAAAGAAAGATCATCAAAGTAGAAATTTGAAATA
TGCTTCCTGGAAGGAATTCTCTGATTTTCATGAAGTGGTCCATTCCTGCCTTTCTTTATTTCC
TGGATAACTTGATTGTCTTCTATGTCCTGTCTATCTTCAACCAGCCATGGCTGTTATCTTC
TCAAATTTTAGCATTATAACAACAGCTCTTCTATTTCAGGATAGTGCTGAAGAGGCGTCTAA
CTGGATCCAGTGGGCTTCCTCCTGACTTTATTTTTGTCTATTGTGGCCTTGACTGCCGGGA
CTAAAACTTTA

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGGCCGGCTTGGCTAGCGCGCGGCGGCC
GTGGCTAAGGCTGCTACGAAGCGAGCTTGGGAGGAGCAGCGGCCTGCGGGGCAGAGGAGCAT
CCCGTCTACCAGGTCCCAAGCGGCGTGGCCCGCGGGTCATGGCCAAAGGAGAAGGCGCCGAG
AGCGGCTCCGCGGCGGGGCTGCTACCCACCAGCATCCTCAAAGCACTGAACGCCCGGCCCA
GGTGAAGAAAGAACCGAAAAAGAAACAACAGTTGTCTGTTTGAACAAGCTTTGCTATG
CACTTGGGGGAGCCCCCTACCAGGTGACGGGCTGTGCCCTGGGTTTCTTCCTTCAGATCTAC
CTATTGG**ATG**TGGCTCAGGTGGGCCCTTTCTCTGCCTCCATCATCCTGTTTGTGGGCCGAGC
CTGGGATGCCATCACAGACCCCCCTGGTGGGCCTCTGCATCAGCAAATCCCCCTGGACCTGCC
TGGGTGCGCTTATGCCCTGGATCATCTTCTCCACGCCCCCTGGCCGTCAATTGCCCTACTTCCTC
ATCTGGTTCGTGCCCCGACTTCCCACACGGCCAGACCTATTGGTACCTGCTTTTCTATTGCCT
CTTTGAAACAATGGTCACGTGTTTCCATGTTCCCTACTCGGCTCTCACCATGTTTCATCAGCA
ACCGAGCAGACTGAGCGGGATTCTGCCACCGCCTATCGGATGACTGTGGAAGTGCTGGGCAC
AGTGCTGGGCACGGCGATCCAGGGACAAATCGTGGGCCAAGCAGACACGCCTTGTTTTCCAGG
ACTTCAATAGCTCTACAGTAGCTTCACAAAGTGCCAAACCATAACATGGCACCCTTCACAC
AGGGAAACGCAAAAGGCATACCTGCTGGCAGCGGGGTCATTGTCTGTATCTATATAATCTG
TGCTGTCACTCCTGATCCTGGGCGTGCGGGAGCAGAGAGAACCCTATGAAGCCCAGCAGTCTG
AGCCAATCGCCTACTTCCGGGGCCTACGGCTGGTCATGAGCCACGGCCCATACATCAAACCTT
ATTACTGGCTTCCTCCTCACCTCCTTGGCTTTTCATGCTGGTGGAGGGGAACCTTGTCTTGTT
TTGCACCTACACCTTGGGCTTCCGCAATGAATTCCAGAATCTACTCCTGGCCATCATGCTCT
CGGCCACTTTAACCATTCCCATCTGGCAGTGGTTCTTACCCGGTTTGGCAAGAAGACAGCT
GTATATGTTGGGATCTCATCAGAGTGCCATTTCTCATCTTGGTGGCCCTCATGGAGAGTAA
CCTCATCATTACATATGCGGTAGCTGTGGCAGCTGGCATCAGTGTGGCAGCTGCCTTCTTAC
TACCCTGTTCCATGCTGCCTGATGTCAATTGACGACTTCCATCTGAAGCAGCCCCACTTCCAT
GGAACCGAGCCCATCTTCTTCTCCTTCTATGTCTTCTTCACCAAGTTTGCCTCTGGAGTGT
ACTGGGCATTTCTACCCTCAGTCTGGACTTTGCAGGGTACCAGACCCGTGGCTGCTCGCAGC
CGAACGTGTCAAGTTTACACTGAACATGCTCGTGACCATGGCTCCCATAGTTCTCATCCTG
CTGGGCCTGCTGCTCTTCAAAATGTACCCCATTGATGAGGAGAGGCGGCGGCAGAATAAGAA
GGCCCTGCAGGCACTGAGGGACGAGGCCAGCAGCTCTGGCTGCTCAGAAACAGACTCCACAG
AGCTGGCTAGCATCCTC**TAG**GGCCCCGCCACGTTGCCCGAAGCCACCATGCAGAAGGCCACAG
AAGGGATCAGGACCTGTCTGCCGGCTTGTGAGCAGCTGGACTGCAGGTGCTAGGAAGGGAA
CTGAAGACTCAAGGAGGTGGCCAGGACACTTGTGTGCTCACTGTGGGGCCGGCTGCTCTG
TGGCCTCCTGCCTCCCCCTCTGCCTGCCTGTGGGGCCAAGCCCTGGGGCTGCCACTGTGAATA
TGCCAAGGACTGATCGGGCCTAGCCCGGAACACTAATGTAGAAACCTTTTTTTTTTACAGAGCC
TAATTAATAACTTAATGACTGTGTACATAGCAATGTGTGTGTATGTATATGTCTGTGAGCTA
TTAATGTTATTAATTTTCATAAAAGCTGGAAAGC

FIGURE 12

MWLRWALS LPPSSCLWAEPGMPSQTPWWASASANPPGPAWVALCPGSSSPRPWPSLPTSSSG
SCPTSHTARPIGT CFSIASLKQWSRVSMFPTRLSPCSSATEQTERDSATAYRMTVEVLGTVL
GTAIQQQIVGQADTPCFQDFNSSTVASQSANHTHGTTSHRETQKAYLLAAGVIVCIYIICAV
ILILGVREQREPYEAQQSEPIAYFRGLRLVM SHGPYIKLITGFLFTSLAFMLVEGNFVLFCT
YTLGFRNEFQNL LLAIMLSATLTIPWQWFLTRFGKKTAVYVGISSAVPFLILVALMESNLI
ITYAVAVAAGISVAAAFLLPWSMLPDVIDDFHLKQPHFHGTEPIFFSFYVFFTKFASGVSLG
ISTLSLDFAGYQTRGCSQPERVKFTLNMLVTMAPIVLILLGLLLFKMYPIDEERRRQNK KAL
QALRDEASSSGCSETDSTELASIL

T09T "T3T650

GGGAAACGCAAAGGCATACCTGCTGGCAGCGGGGGTCATTGTCTGTATCTATATAATCTGT
GCTGTCATCCTGATCCTGGGCGTGCGGGAGCAGAGAGAACCCTATGAAGCCCAGCAGTCTGA
GCCAATCGCCTACTTCCGGGGCCTACGGCTGGTCATGAGCCACGGCCCATACATCAAACCTTA
T TACTGGCTTCCTCTTCACCTCCTTGGCTTTTCATGCTGGTGGAGGGGAACTTTGTCTTGTTT
TGCACCTACACCTTGGGCTTCCGCAATGAATTCCAGAATCTACTCCTGGCCATCATGCTCTC
GGCCACTTTAACCATTCCCATCTGGCAGTGGTTCTTGACCCGGTTTGGCAAGAAGACAGCTG
TATATGTTGGGATCTCATCAGCAGTGCCATTTCTCATCTTGGTGGCCCTCATGGAGAGTAAC
CTCATCATTACATATGCGGTAGCTGTGGCAGCTGGCATCAGTGTGGCAGCTGCCTTCTTACT
ACCCTGGTCCATGCTGCCTGATGTCATTGACGACTTCCATCTGAAGCAGCCCCACTTCCATG
GAACCGAGCCCAT

GGGGCTTCGGCGCCAGCGGCCAGCGCTAGTCTGGTAAGGATTTACAAAAGGTGCAGGT
ATGAGCAGGTCTGAAGACTAACATTTTTGTGAAGTTGTAAAACAGAAAACCTGTTAGAAATGT
GGTGGTTTTAGCAAGGCCTCAGTTTCCTTCCTTCAGCCCTTGTAATTTGGACATCTGCTGCT
TTCATATTTTCATACATTACTGCAGTAACACTCCACCATATAGACCCGGCTTTACCTTATAT
CAGTGACACTGGTACAGTAGCTCCAGAAAAATGCTTATTTGGGGCAATGCTAAATATTGCGG
CAGTTTTATGCATTGCTACCATTTATGTTTCGTTATAAGCAAGTTCATGCTCTGAGTCCTGAA
GAGAACGTTATCATCAAATTAACAAGGCTGGCCTTGTAAGTGGGCAATGCTAAATATTGCGG
ACTTTCTATTGTGGCAAACCTTCAGAAAAACAACCCTTTTTGCTGCACATGTAAGTGGAGCTG
TGCTTACCTTTGGTATGGGCTCATTATATATGTTTGTTTCAGACCATCCTTTCCTACCAAATG
CAGCCCCAAAATCCATGGCAAACAAGTCTTCTGGATCAGACTGTTGTTGGTTATCTGGTGTGG
AGTAAGTGCACCTTAGCATGCTGACTTGCTCATCAGTTTTGCACAGTGGCAATTTTGGGACTG
ATTTAGAACAGAACTCCATTGGAACCCCGAGGACAAAGGTTATGTGCTTCACATGATCACT
ACTGCAGCAGAATGGTCTATGTCATTTTCCTTCTTTGGTTTTTTCCTGACTTACATTCTGTA
TTTTTCAGAAAATTTCTTTACGGGTGGAAGCCAATTTACATGGATTAACCCTCTATGACACTG
CACCTTGCCCTATTAACAATGAACGAACACGGCTACTTTCCAGAGATATTTTGATGAAAGGAT
AAAATATTTCTGTAATGATTATGATTCTCAGGGATTGGGGAAAGGTTACAGAAAGTTGCTTA
TTCTTCTCTGAAATTTTCAACCACTTAATCAAGGCTGACAGTAACACTGATGAATGCTGATA
ATCAGGAAACATGAAAGAAGCCATTTGATAGATTATTCTAAAGGATATCATCAAGAAGACTA
TTAAAAACACCTATGCCTATACTTTTTTATCTCAGAAAATAAAGTCAAAGACTATG

MWWFQOGLSFLPSALVIWTSAAFI FSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAMLNI
AAVLCIATIYVRYKQVHALSPEENVIIKLNKAGLVLGILSCLGLSIVANFQKTTLFAAHVSG
AVLTFGMGSLYMFVQTILSYQMOPKIHGKQVFWIRLLLVIWCGVSALSMLTCSSVLHSGNFG
TDLEQKLHWNPEDKGYVLHMITTAAEWSMSFSFFGGFFLT YIRDFQKISLRVEANLHGLTLYD
TAPCPINNERTRLLSRDI

FIGURE 16

CGGACGCTTGGGCNGCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGTGCCTGATGCCGAGT
TCCGTCTCTCGGGTCTTTTCCTGGTCCCAGGCAAAGCGGAGCGGAGATCCTCAAACGGCCTA
GTGCTTCGCGCTTCCGGAGAAAATCAGCGGTCTAATTAATTCCTCTGGTTTGTGGAAGCAGT
TACCAAGAATCTTCAACCCTTTCCCACAAAAGCTAATTGAGTACACGTTCCCTGTTGAGTACA
CGTTCCTGTTGATTTACAAAAGGTGCAGGTATGAGCAGGTCTGAAGACTAACATTTTGTGAA
GTTGTAAAACAGAAAACCTGTTAGAAATGTGGTGGTTTCAGCAAGGCCTCAGTTTCCTTCCT
TCAGCCCCTTGTAATTTGGACATCTGCTGCTTTCATATTTTCATACATTACTGCAGTAACACT
CCACCATATAGACCCGGCTTTACCTTATATCAGTGACACTGGTACAGTANC

FIGURE 17

CCCACGCGTCCGCCCCGCGCTGCGTCCCGGAGTGCAAGTGAGCTTCTCGGCTGCCCCGCGGG
CCGGGGTGCGGAGCCGACATGCGCCCCGCTTCTCGGCCTCCTTCTGGTCTTCGCCGGCTGCAC
CTTCGCCTTGTACTTGCTGTGACGCGACTGCCCCGCGGGCGGAGACTGGGCTCCACCGAGG
AGGCTGGAGGCAGGTGCTGTGGTTCCCCCTCCGACCTGGCAGAGCTGCGGGAGCTCTCTGAG
GTCCTTCGAGAGTACCGGAAGGAGCACCAGGCCTACGTGTTCTTGCTCTTCTGCGGCGCCTA
CCTCTACAAACAGGGCTTTGCCATCCCCGGCTCCAGCTTCCTGAATGTTTTAGCTGGTGCCT
TGTTTTGGGCCATGGCTGGGGCTTCTGCTGTGCTGTGTGTTGACCTCGGTGGGTGCCACATGC
TGCTACCTGCTCTCCAGTATTTTTGGCAAACAGTTGGTGGTGTCTACTTTCTGATAAAGT
GGCCCTGCTGCAGAGAAAGGTGGAGGAGAACAGAAACAGCTTGTTTTTTTTCTTATTGTTTT
TGAGACTTTTCCCCATGACACCAAACCTGGTTCTTGAACCTCTCGGCCCCAATTCTGAACATT
CCCATCGTGCAGTTCTTCTTCTCAGTTCTTATCGGTTTGATCCCATATAATTTTCATCTGTGT
GCAGACAGGGTCCATCCTGTCAACCCTAACCTCTCTGGATGCTCTTTTCTCCTGGGACACTG
TCTTTAAGCTGTTGGCCATTGCCATGGTGGCATTAATTCCTGGAACCCCTCATTAAAAAATTT
AGTCAGAAACATCTGCAATTGAATGAAACAAGTACTGCTAATCATATACACAGTAGAAAAGA
CACATTGATCTGGATTTTCTGTTTGCCACATCCCTGGACTCAGTTGCTTATTTGTGTAATGGA
TGTGGTCCTCTAAAGCCCCTCATTGTTTTTGATTGCCTTCTATAGGTGATGTGGACACTGTG
CATCAATGTGCAGTGTCTTTTCAGAAAGGACACTCTGCTCTTGAAGGTGTATTACATCAGGT
TTTCAAACCAGCCCTGGTGTAGCAGACACTGCAACAGATGCCTCCTAGAAAATGCTGTTTGT
GGCCGGGCGCGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCCGGTGATTC
ACAAGGTCAGGAGTTCAAGACCAGCCTGGCCAAGATGGTGAAATCCTGTCTCTAATAAAAAT
ACAAAAATTAGCCAGGCGTGGTGGCAGGCACCTGTAATCCCAGCTACTCGGGAGGCTGAGGC
AGGAGAATTGCTTGAACCAAGGTGGCAGAGGTTGCAGTAAGCCAAGATCACACCACTGCACT
CCAGCCTGGGTGATAGAGTGAGACACTGTCTTGAC

FIGURE 18

MRPLLGLLLVFAGCTFALYLLSTRLPGRRLGSTEEAGGRSLWFPSDLAELREELSEVLREYR
KEHQAYVFLLFCGAYLYKQGFAIPGSSFLNVLAGALFGPWLGLLLCCVLTSGATCCYLLSS
IFGKQLVVSYPDKVALLQRKVEENRNSLFFFLFLRLFPMTPNWFLNLSAPILNIPIVQFF
FSVLIGLIPYNFICVQTGSILSTLTSLDALEFSWDTVFKLLAIAMVALIPGTLIKKFSQKHLQ
LNETSTANHIHSRKDT

Important features:

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 101-123, 189-211

N-glycosylation sites.

amino acids 172-176, 250-254

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 240-244, 261-265

N-myristoylation site.

amino acids 13-19, 104-110, 115-121, 204-210

Amidation site.

amino acids 27-31

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 4-15

Protein splicing proteins.

amino acids 25-31.

Sugar transport proteins.

amino acids 162-172

FIGURE 19

CCGAGGCGGGAGGAGCCCGAGGGGGCGCGAGCCCCGCATGAATCATTGTAGTCAATCATTTTT
CCAGTTCTCAGCCGCTCAGTTGTGATCAAGGGACACGTGGTTTCCGAAC TGCCAGCTCAGAA
TAGGAAAATAACTTGGGATTTTATATTGGAAGAC **ATG**GATCTTGCTGCCAACGAGATCAGCA
TTTATGACAACTTTCAGAGACTGTTGATTTGGTGAGACAGACCGGCCATCAGTGTGGCATG
TCAGAGAAGGCAATTGAAAAATTTATCAGACAGCTGCTGGAAAAGAATGAACCTCAGAGACC
CCCCCGCAGTATCCTCTCCTTATAGTTGTGTATAAGGTTCTCGCAACCTTGGGATTAATCT
TGCTCACTGCCTACTTTGTGATTCAACCTTTCAGCCCATTAGCACCTGAGCCAGTGCTTTCT
GGAGCTCACACCTGGCGCTCACTCATCCATCACATTAGGCTGATGTCCTTGCCCATTGCCAA
GAAGTACATGTCAGAAAATAAGGGAGTTCCTCTGCATGGGGGTGATGAAGACAGACCCTTTC
CAGACTTTGACCCCTGGTGGACAAACGACTGTGAGCAGAATGAGTCAGAGCCCATTCTGCC
AACTGCACTGGCTGTGCCCAGAAACACCTGAAGGTGATGCTCCTGGAAGACGCCCCAAGGAA
ATTTGAGAGGCTCCATCCACTGGTGATCAAGACGGGAAAGCCCCTGTTGGAGGAAGAGATTC
AGCATTTTTTGTGCCAGTACCCTGAGGCGACAGAAGGCTTCTCTGAAGGGTTTTTCGCCAAG
TGGTGGCGCTGCTTTCTGAGCGGTGGTTCCCATTTCTTATCCATGGAGGAGACCTCTGAA
CAGATCACAAATGTTACGTGAGCTTTTTCTGTCTTCACTCACCTGCCATTTCCAAAAGATG
CCTCTTTAAACAAGTGCTCCTTTCTTCACCCAGAACCTGTTGTGGGGAGTAAGATGCATAAG
ATGCCTGACCTATTTATCATTGGCAGCGGTGAGGCCATGTTGCAGCTCATCCCTCCCTTCCA
GTGCCGAAGACATTGTCAGTCTGTGGCCATGCCAATAGAGCCAGGGGATATCGGCTATGTGCG
ACACCACCCACTGGAAGGTCTACGTTATAGCCAGAGGGGTCCAGCCTTTGGTCATCTGCGAT
GGAACCGCTTTCTCAGAACTG **TAG**GAAATAGA ACTGTGCACAGGAACAGCTTCCAGAGCCGA
AAACCAGGTTGAAAGGGGAAAAATAAAAACAAAACGATGAAACTGCAAAAA

FIGURE 20

MDLAANEISIIYDKLSETVDLVRQTGHQCGMSEKAIEKFIRQLLEKNEPQRPPQYPLLIVVY
KVLATLGLILLTAYFVIQPFSPLAPEPVLSGAHTWRSLIHHIRLMSLPIAKKYMSENKGVPL
HGGDEDRPFPDFDPWWTNDCEQNESEPIPANCTGCAQKHLKVMLLEDAPRKFERLHPLVIKT
GKPLLEEEIQHFLCQYPEATEGFSEGFFAKWWRCFPERWFPFPYRWRRPLNRSQMLRELFV
FTHLPFPKDASLNKCSFLHPEPVVGSKMHKMPDLFIIGSGEAMLQLIPPFQCRHRCQSVAMP
IEPGDIGYVDTTHWKVYVIARGVQPLVICDGTAFSEL

0994181 11601
TOSTT "TBT66D

FIGURE 21

CCACGGTGTCCGTTCTTCGCCCCGGCGGCAGCTGTCCCCGAGGCGGGAGGAGCCCCGAGGGGCG
CGAGCCCCGCATGAATCATTGTAGTCAATCATTTTCCAGTTCTCAGCCGTTTCAGTTGTGATC
AAGGGACACGTGGTTTTCCGAACTGCCAGCTCAGAATAGGAAAATAACTTGGGATTTTATATT
GGAAGACATGGATCTTGCTGCCAACGAGATCAGCATTTATGACAACTTTCAGAGACTGTTG
ATTTGGTGAGACAGACCGGCCATCAGTGTGGCATGTCAGAGAAGGCAATTGAAAAATTTATC
AGACAGCTGCTGGAAAAGAATGAACCTCAGAGACCCCCCGCAGTATCCTCTCCTTATAGT
TGTGTATAAGGTTCTCGCAACCTTGGGATTAATCTTGCTCACTGCCTACTTTGTGATTCAAC
CTTTCAGCCCATTAGCACCTGAGCCAGTGCTTTGTGGAGCTCAC

CCACGCGTCCGCCACGCGTCCGGCTGAACACCTCTTCTTTGGAGTCAGCCACTGATGAGG
CAGGCTCCCCACTTGCAGCTGCAGCAGCTGCAGAGCGCTGCTCCTGGCTGGTG
CCACTGGTGCGCACGCTGCTAGACCGTGCCATATGAGCCGCTGGGGCTGCAGTGGGGACTGCC
CTCCCTGCCACCCACCAATGGCAGCCCCACCTTCTTTGAAGACTTCCAGGCTTTTTTGTGCCA
CACCCGAATGGCGCCACTTTCATCGACAAACAGGTACAGCCAACCATGCTCCAGTTTCGAAATG
GACACGTATGCTAAGAGCCACGACCTTATGTCAAGTTTCTGGAATGCCTGCTATGACATGCT
TATGAGCAGTGGGCGACGGCGCCAGCTGGGAGCGCGCCAGAGTCGTGCGGGCCTTCCAGGAGC
TGGTGCTGGAACCTGCGCAGAGGCGGGCGCGCCTGGAGGGGCTACGCTACACGGCAGTGCTG
AAGCAGCAGGCAACGCAGCACTCCATGGCCCTGCTGCAGTGGGGGGCGCTGTGGCGGCCAGCT
CGCCAGCCCATGTGGGGCCTGGGCGCTGAGGGACACTCCCATCCCCGCTGGAAACTGTCCA
GCGCCGAGACATATTCACGCATGCTCTGAAGCTGGTGCCCAACCATCACTTCGACCCCTCAC
CTGGAAGGACGCGCTCTCCGAGACAACTCTGGGTGAGGTTCCCTGACACCCACCGAGGAGGC
CTCACTGCCTCTGGCAGTGACCAAAGAGGCCAAAGTGAGCACCCACCCGAGTTGCTGCAGG
AGGACCAGCTCGGCGAGGACGAGCTGGCTGAGCTGGAGACCCCGATGGAGGCGAGCAGAACTG
GATGAGCAGCGTGAGAAGCTGGTGCTGTGCGCCGAGTGCCAGCTGGTGACGGTAGTGGCCGT
GGTCCCAGGGCTGCTGGAGGTCAACACAGAAATGTATACTTCTACGATGGCAGCACTGAGC
GCGTGGAAACCGGAGGAGGCGATCGGCTATGATTTCCGGCGCCCACTGGCCCAGCTGCGTGAG
GTCCACCTGCGGCGTTTCAACCTGCGCCGTTACGCACTTGAGCTCTTCTTTATCGATCAGGC
CAACTACTTCTCAACTTCCCATGCAAGGTGGGCACGACCCCACTCATCTCCTAGCCAGA
CTCCGAGACCCCGAGCTGGCCCCATCCCACCCCATACCCAGGTACGGAACCAAGGTGTACTCG
TGGCTCCTGCGCCTACGGCCCCCTCTCAAGGCTACCTAAGCAGCGCTCCCCCGAGGAGAT
GCTGCGTGCCTCAGGCTTACCCAGAAATGGGTACAGCGTGAGATATCCAACCTTCGAGTACT
TGATGCAACTCAACACCATTGCGGGGCGGACCTACAATGACCTGTCTCAGTACCCTGTGTTC
CCCTGGGTCTGTCAGGACTACGTGTCCCCAACCCCTGGACCTCAGCAACCCAGCCGTCTTCCG
GGACCTGTCTAAGCCCATCGGTGTGGTGAACCCCAAGCATGCCAGCTCGTGAGGGAGAAGT
ATGAAGCTTTGAGACCCAGCAGGGACATTGACAAGTTCCACTATGGCACCCTACTACTC
AATGACGAGGCGTGATGCACTACCTCATCCGCGTGGAGCCCTTCACTCCCTGCACGTCCA
GCTGCAAAGTGCCGCTTTGACTGCTCCGACCGGCAGTTCCACTCGGTGGCGGCAGCCTGGC
AGGCACGCTGGAGAGCCCTGCCGATGTGAAGGAGCTCATCCCGGAATTCTTCTACTTTCT
GACTTCTTGAGAAACCAGAACGGTTTTGACCTGGGCTGTCTCCAGCTGACCAACGAGAAGT
AGGCGATGTGGTGCTACCCCGTGGGCGAGCTCTCCTGAGGACTTCATCCAGCAGCACC
AGGCTCTGGAGTCTCGAGTATGTGTCTGCACACCTACACGAGTGGATCGACCTCATCTTTGGC
TACAAGCAGCGGGGGCCAGCCGCGGAGGAGGCCCTCAATGTCTTCTATTACTGCACCTATGA
GGGGGCTGTAGACCTGGACCATGTGACAGATGAGCGGGAACGGAAGGCTCTGGAGGGCATT
TCAGCAACTTTGGGCAGACTCCCTGTGACGTGCTGAAGGAGCCACATCCAACCTCGGCTCTCA
GCTGAGGAAGCAGCCCATCGCTTGACAGCCTGGACACTAACTACCTAGCATCTTCCAGCA
CCTGGACGAACCTCAAGGCATTCTTTCGACAGAGGTGACTGTGAGTGCCAGTGGGCTGCTGGGCA
CCCACAGCTGGTTGCCCTATGACCGCAACATAAGCAACTACTTCAGCTTCAGCAAAGACCCC
ACCATGGGCAGCCACAAGACGCGAGCTGCTGAGTGGCCCGTGGGTGCCAGGCACTGGTGT
GAGTGGACAAGCACTGGCAGTGGCCCCGATGGAAGCTGCTATTACGCGGTGGCCACTGGG
ATGGCAGCTGCGGGTGACTGCACTACCCCGTGGCAAGCTGTTGAGCCAGCTCAGCTGCCAC
CTTGATGTAGTAACCTGCCTTGCACTGGACACCTGTGGCATCTACCTCATCTCAGGCTCCCG
GGACACCACGTGCATGGTGTGGCGGCTCCTGCATCAGGGTGGTCTGTGATAGGCCTGGCAC
CAAAGCCTGTGACGGTCTGTATGGGCATGGGGCTGCAGTGAGCTGTGTGGCCATCAGCACT
GAACTTGACATGGCTGTGTCTGAGTGTGAGGATGGAAGTGTGATCATACACACTGTACGCCG
CGGACAGTTTGTAGCGGCACTACGCCCTCTGGGTGCCACATTCCCTGGACCTATTTTCCACC
TGGCATTTGGGGTCCGAAGGCCAGATTGTGGTACAGAGCTCAGCGTGGGAACGTCTGGGGCC
CAGGTACCTACTCCTTGCACCTGTATTGAGTCAATGGGAAGTTGCGGGGCTTCACTGCCCT
GGCAGAGCAGCTACAGCCCTGACGGTGACAGAGGACTTTGTGTGTGGGACCGCCAGT
GCGCCCTGACATCTTCCAACATAAACACACTGCTCCCGGGCGCGCTCCCTTGCCCATGAAG
GTGGCCATCCGCAGCGTGGCCGTGACCAAGGAGCGCAGCCACGTGCTGGTGGGCCTGGAGGA
TGGCAAGCTCATCGTGGTGGTTCGCGGGGCGAGCCCTCTGAGGTGCGCAGCAGCCAGTTCGCGC
GGAAGCTGTGGCGGTCTCTCGCGGCGCATCTCCAGGTGTCTCGGGAGAGACGGAATACAAC
CCTACTGAGGCGCGCTGGAACCTGGCCAGTCCGGCTGCTCGGGCCCCCGCCCGCAGCCCTG
GCCCGGGAGGCCCCGCCAGAAGTCGGCGGGAACACCCCGGGTGGGCAGCCAGGGGGTGA
GCGGGGCCACCTCTGCCAGACTCAGGGATTGGCGGGCGCATGTTACCCCTCAGGGATTGGCG
GGCGGAAGTCCCGCCCCCTCGCGGGCTGAGGGGCGGCCCTGAGGGCCAGCACTGGCGTCT

FIGURE 23

MSQFEMDTYAKSHDLMSGFWNACYDMLMSSGQRRQWERAQSRRAFQELVLEPAQRRARLEGL
 RYTAVLKQQATQHSMALLHWGALWRQLASPCGAWALRDTPIPRWKLSSAETYSRMRLKLVNP
 HHFDPHLEASALRDNLGEVPLTPTEEASLPLAVTKEAKVSTPPELLQEDQLGEDELAELETP
 MEAAELDEQREKLVLSAECQLVTVVAVVPGLLLEVTTQNVYFYDYGSTERVETEEGIGYDFRRP
 LAQLREVHLRRFNLRRSALELFFIDQANYFLNFPCKVGTTPVSSPSQTPRPQPGPIPPHTQV
 RNQVYSWLLRLRPPSQGYLSSRSPQEMLRASGLTQKWVQREISNFEYLMQLNTIAGR TYNDL
 SQYPVFPWVLQDYVSPTLDLSNPAVFRDLSKPIGVVNPKHAQLVREKYESFEDPAGTIDKFH
 YGTHYSNAAGVMHYLIRVEPFTSLHVQLQSGRFDCSDRQFHSVAAAWQARLESPADV KELIP
 EFFYFPDFLENQNGFDLGCLQLTNEKVGDVVLPPWASSPEDFIQQHRQALESEYVSAHLHEW
 IDLIFGYKQRGPAEEALNVFYYCTYEGAVDLDHVTDERERKALEGIIISNFGQTPCQLLKEP
 HPTRLSAEEAAHRLARLDTNSPSIFQHLDELKAFFAEVTVSASGLLGTHSWLPYDRNISNYF
 SFSKDPTMGSHKTQRLLSGPWVPVSGSVSGQALAVAPDGKLLFSGGHWGSLRVTALPRGKLL
 SQLSCHLDVVTCALDTCGIY LISGSRDTTCMVWRLLHQGGLSVGLAPKPVQVLYGHGA AVS
 CVAISTELDMAVSGSEDGTVIIHTVRRGQFVAALRPLGATFPGP I FHLALGSEGQIVVQSSA
 WERPGAQVTYSLHLYSVNGKLRASLPLAEQPTALTVTEDFVLLGTAQCALHILQLNTLLPAA
 PPLPMKVAIRSVAVTKERSHVLVGLEDGKLIVVAGQPSEVRSSQFARKLWRSSRRISQVSS
 GETEYNPTEAR

N-glycosylation site.

amino acids 677-681

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 985-989

Tyrosine kinase phosphorylation site.

amino acids 56-65, 367-376, 543-551

N-myristoylation site.

amino acids 61-67, 436-442, 604-610, 610-616, 664-670, 691-697,
 706-712, 711-717, 769-775, 785-791, 802-808, 820-826, 834-840,
 873-879, 912-918, 954-960

FIGURE 24

CGGACGCGTGGGCGGACGCGTGGGGGCTGTGAGAAAGTGCCAATAAATACATCATGCAACCC
CACGGCCACCTTGTGAACTCCTCGTGCCAGGGCTGATGTGCGTCTTCCAGGGCTACTCAT
CCAAAGGCCATAATCCAACGTTCTGTCTTCAATCTGCAAATCTATGGGGTCTTGGGGCTCTTC
TGGACCCCTTAAGTGGGTACTGGCCCTGGGCCAATGCGTCCTCGCTGGAGCCTTGCCTCCTT
CTACTGGGCCTTCCACAAGCCCCAGGACATCCCTACCTTCCCCCTTAATCTCTGCCTTCATCC
GCACACTCCGTTACCACACTGGGTCATTGGCATTGGAGCCCTCATCCTGACCCTTGTGCAG
ATAGCCCGGGTCATCTTGGAGTATATTGACCACAAGCTCAGAGGAGTGCAGAACCCTGTAGC
CCGCTGCATCATGTGCTGTTTCAAGTGCTGCCTCTGGTGTCTGGAAAAATTTATCAAGTTCC
TAAACCGCAATGCATACATCATGATCGCCATCTACGGGAAGAATTTCTGTGTCTCAGCCAAA
AATGCGTTCATGCTACTCATGCGAAACATTGTCAGGGTGGTCGTCTGGACAAAGTCACAGA
CCTGCTGCTGTTCTTTGGGAAGCTGCTGGTGGTCGGAGGCGTGGGGGTCCTGTCCTTCTTTT
TTTTCTCCGGTCGCATCCCGGGGCTGGGTAAAGACTTTAAGAGCCCCCACCTCAACTATTAC
TGGCTGCCCATCATGACCTCCATCCTGGGGGCCTATGTCATCGCCAGCGGCTTCTTCAGCGT
TTTCGGCATGTGTGTGGACACGCTCTTCTCTGCTTCCTGGAAGACCTGGAGCGGAACAACG
GCTCCCTGGACCGGCCCTACTACATGTCCAAGAGCCTTCTAAAGATTCTGGGCAAGAAGAAC
GAGGCGCCCCCGGACAACAAGAAGAGGAAGAAG**TGAC**AGCTCCGGCCCTGATCCAGGACTGC
ACCCACCCCCACCGTCCAGCCATCCAACCTCACTTCGCCTTACAGGTCTCCATTTTGTGGT
AAAAAAGGTTTTAGGCCAGGCGCCGTGGCTCACGCCTGTAATCCAACACTTTGAGAGGCTG
AGGCGGGCGGATCACCTGAGTCAGGAGTTCGAGACCAGCCTGGCCAACATGGTGAAACCTCC
GTCTCTATTAAAAATACAAAATTAGCCGAGAGTGGTGGCATGCACCTGTCATCCCAGCTAC
TCGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTGAGCCGAGA
TCGCGCCACTGCACTCCAACCTGGGTGACAGACTCTGTCTCCAAAACAAAACAAACAAACAA
AAAGATTTTATTAAAGATATTTTGTTAACTC

RTRGRTRGGCEKVPINTSCNPHTAHLVNSSCPGLMCVFQGYSSKGLIQRSVFNLQIYGVLGLEF
WTLNWVLALGQCVLAGAFASFYWAFHKPQDIPTFPLISAFIRTLRYHTGSLAFGALILTIVQ
IARVILEYIDHKLRGVQNPVARCIMCCFKCCLWCLEKFIKFLNRNAYIMIAIYGKNFCVSAK
NAFMLLMRNIVRVVLDKVTDLLLFFGKLLVVGGVGVLSFFFFSGRIPGLGKDFKSPHLNYY
WLPIMTSILGAYVIASGFFSVFGMCVDTLFLCFLEDLERNNGSLDRPYYSKSLKILGKKN
EAPPDNKKRKK

FIGURE 26

GAGTCTTGACCGCCGCCGGGCTCTTGGTACCTCAGCGCGAGCGCCAGGCGTCCGGCCGCCGT
GGCT**ATG**TTTCGTGTCCGATTTCCGCAAAGAGTTCTACGAGGTGGTCCAGAGCCAGAGGGTCC
TTCTCTTCGTGGCCTCGGACGTGGATGCTCTGTGTGCGTGCAAGATCCTTCAGGCCTTGTTTC
CAGTGTGACCACGTGCAATATACGCTGGTTCCAGTTTCTGGGTGGCAAGAACTTGAAACTGC
ATTTCTTGAGCATAAAGAACAGTTTCATTATTTTATTCTCATAAACTGTGGAGCTAATGTAG
ACCTATTGGATATTCTTCAACCTGATGAAGACACTATATTCTTTGTGTGTGACTCCCATAGG
CCAGTCAATGTCGTCAATGTATACAACGATACCCAGATCAAATTACTCATTAAACAAGATGA
TGACCTTGAAGTTCCCGCCTATGAAGACATCTTCAGGGATGAAGAGGAGGATGAAGAGCATT
CAGGAAATGACAGTGATGGGTGAGAGCCTTCTGAGAAGCGCACACGGTTAGAAGAGGAGATA
GTGGAGCAAACCATGCGGAGGAGGCAGCGGCGAGAGTGGGAGGCCCGGAGAAGAGACATCCT
CTTTGACTACGAGCAGTATGAATATCATGGGACATCGTCAGCCATGGTGATGTTTGAGCTGG
CTTGATGCTGTCCAAGGACCTGAATGACATGCTGTGGTGGGCCATCGTTGGACTAACAGAC
CAGTGGGTGCAAGACAAGATCACTCAAATGAAATACGTGACTGATGTTGGTGTCTTGCAGCG
CCACGTTTCCCGCCACAACCACCGGAACGAGGATGAGGAGAACACACTCTCCGTGGACTGCA
CACGGATCTCCTTTGAGTATGACCTCCGCCTGGTGCTCTACCAGCACTGGTCCCTCCATGAC
AGCCTGTGCAACACCAGCTATACCGCAGCCAGGTTCAAGCTGTGGTCTGTGCATGGACAGAA
GCGGCTCCAGGAGTTCCTTGACAGACATGGGTCTTCCCTGAAGCAGGTGAAGCAGAAGTTCC
AGGCCATGGACATCTCCTTGAAGGAGAATTTGCGGGAAATGATTGAAGAGTCTGCAAATAAA
TTTGGGATGAAGGACATGCGCGTGCAGACTTTCAGCATTCAATTTGGGTTCAGCACAAGTT
TCTGGCCAGCGACGTGGTCTTTGCCACCATGTCTTTGATGGAGAGCCCCGAGAAGGATGGCT
CAGGGACAGATCACTTCATCCAGGCTCTGGACAGCCTCTCCAGGAGTAACCTGGACAAGCTG
TACCATGGCCTGGAACCTGCCAAGAAGCAGCTGCGAGCCACCCAGCAGACCATTGCCAGCTGC
CTTTGCACCAACCTCGTCATCTCCAGGGGCCTTTCTGTACTGCTCTCTCATGGAGGGCAC
TCCAGATGTCATGCTGTTCTCTAGGCCGGCATCCCTAAGCCTGCTCAGCAAACACCTGCTCA
AGTCCTTTGTGTGTTTCGACAAAGAACCGGCGCTGCAAACCTGCTGCCCCTGGTGATGGCTGCC
CCCCTGAGCATGGAGCATGGCACAGTGACCGTGGTGGGCATCCCCCAGAGACCGACAGCTC
GGACAGGAAGAACTTTTTTGGGAGGGCGTTTGAGAAGGCAGCGGAAAGCACCAGCTCCCGGA
TGCTGCACAACCATTTTGACCTCTCAGTAATTGAGCTGAAAGCTGAGGATCGGAGCAAGTTT
CTGGACGCACTTATTTCCCTCCTGTCC**TAG**GAATTTGATTCTTCCAGAATGACCTTCTTATT
TATGTAACCTGGCTTTCATTTAGATTGTAAGTTATGGACATGATTTGAGATGTAGAAGCCATT
TTTTATTAAATAAAATGCTTATTTTAGGAAA

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FIGURE 27

MFVSDFRKEFYEVVQSQRVLLFVASDVDALCACKILQALFQCDHVQYTLVPVSGWQELETAF
LEHKEQFHYFILINCGANVDLLDILQPDEDTIFFVCDSHRPVNVVNVYNDTQIKLLIKQDDD
LEVPAYEDIFRDEEEDEEHSGNDSGSEPSEKRTRLEEEIVEQTMRRRQRREWEARRRDILF
DYEQYEHGTSSAMVMFELAWMLSKDLNDMLWWAIVGLTDQWVQDKITQMKYVTDVGVLQRH
VSRHNRNEDEENTLSVDCTRISFEYDLRLVLYQHWSLHDSL CNTSYTAARFKLWSVHGQKR
LQEF LADMGLPLKQVKQKFQAMDISLKENLREMIEESANKFGMKDMRVQTF SIHFGFKHKFL
ASDVVFATMSLMESPEKDGSGTDHFIQALDSLRSNLDKLYHGLELAKKQLRATQQTIASCL
CTNLVISQGPFLYCSLMEGTPDVMLFSRPASLSLLSKHLLKSFVCSTKNRRCKLLPLVMAAP
LSMEHGTVTVVGIPPETDSSDRKNFFGRAFEKAAESTSSRMLHNHFDLSVIELKAEDRSKFL
DALISLLS

1.0311.1.31.660

FIGURE 28

GTACCTCAGCGCGAGCGCCAGGCGTCCGGCCGCCGTGGCTATGNTCGTGTCCGATTTCCGCA
AAGAGTTCTACGAGGTGGTCCAGAGCCAGAGGGTCCTTCTCTTCGTGGCCTCGGANGTGGAT
GCTCTGTGTGCGTGCAAGATCCTTCAGGCCTTGTTCCAGTGTGACCANGTGCAATATANGCT
GGTTCAGTTTCTGGGTGGCAAGAACTTGAACTGCATTTCTTGAGCATAAAGAACAGTTTC
ATTATTTTATTCTCATAAACTGTGGAGCTAATGTAGACCTATTGGATATTCTTCAACCTGAT
GAAGACACTATATTCTTTGTGTGTGACACCCATAGGCCAGTCAATGTTGTCAATGTATACAA
CGATACCC

T.C.G.T.T."T.E.T.T.S.S.D

FIGURE 29

CAGGAACCCCTCTCTTTGGGTCTGGATTGGGACCCCTTTCCAGTACCATTTTTTCTAGTGAAC
 CACGAAGGGACGATACCAGAAAAACACCCTCAACCCAAAGGAAATAGACTACAGCCCCAATTG
 GCTGACTTTGGCTATAGAAAAAAGAAAGGAACGAAAAGAGACAGTTTTTTTTTGGAAAGCTAA
 GTCTTCCCTTTATCGAGTCAAGAAACCCCCCTTCTTGAGCTATTTACAGCTTTTAAACAATT
 GAGTAAAGTACGCTCCGGTCAACC**ATGGT**GACAGCCGCCCTGGGTCCCGTCTGGGCAGCGCTC
 CTGCTCTTTCTCCTGATGTGTGAGATCCGTATGGTGGAGCTCACCTTTGACAGAGCTGTGGC
 CAGCGGCTGCCAACGGTGCTGTGACTCTGAGGACCCCTGGATCCTGCCCATGTATCCTCAG
 CCTCTTCCCTCCGGCCGCCCCACGCCCTGCCTGAGATCAGACCCTACATTAATATCACCATC
 CTGAAGGGTGACAAAGGGGACCCAGGCCCAATGGGCCTGCCAGGGTACATGGGCAGGGAGGG
 TCCCCAAGGGGAGCCTGGCCCTCAGGGCAGCAAGGGTGACAAGGGGGAGATGGGCAGCCCCG
 GCGCCCCGTGCCAGAAGCGCTTCTTCGCCCTTCTCAGTGGGCCGCAAGACGGCCCTGCACAGC
 GGCGAGGACTTCCAGACGCTGCTCTTCGAAAGGGTCTTTGTGAACCTTGATGGGTGCTTTGA
 CATGGCGACCGGCCAGTTTGCTGCTCCTCCCTGCGTGGCATCTACTTCTTCAGCCTCAATGTGC
 ACAGCTGGAATTACAAGGAGACGTACGTGCACATTATGCATAACCAGAAAGAGGCTGTATC
 CTGTACGCGCAGCCCAGCGAGCGCAGCATCATGCAGAGCCAGAGTGTGATGCTGGACCTGGC
 CTACGGGGACCGCGTCTGGGTGCGGCTCTCAAGCGCCAGCGCGAGAACGCCATCTACAGCA
 ACGACTTCGACACCTACATCACCTTCAGCGGCCACCTCATCAAGCCGAGAGGACGAC**TGAGGG**
 CCTCTGGGCCACCTCCCGGCTGGAGAGCTCAGGTGCTGGTCCCGTCCCTGCAGGGCTCAG
 TTTGCACTGCTGTGAAGCAGGAAGGCCAGGGAGGTCCCCGGGGACCTGGCATTCTGGGGAGA
 CCCTGCTTCTATCTTGGCTGCCATCATCCCTCCCAGCCTATTTCTGCTCCTCTCTTCTCTCT
 TGGACCTATTTTAAAGAAGCTTGCTAACCTAAATATTTCTAGAACTTTCCCAGCCTCGTAGCCC
 AGCACTTCTCAAACCTTGGAATGCATGCGAATCACCCGGGGTTCGTGTTAAATGCAGATTCT
 GACTCAGCAGGTCTGAGTGGGTCCAGGATTCTGTGTTTCTCATATGTTTCTGGGTGATGCTG
 ATGGGGTCAGTCTATGAACCACACTGGAGCAACCAGGTTCTAGGACTTTCTCAATATTCTAG
 TACTTTCTGAACATTCTGGAATCCTCCCCACATTCTAGAATTCTCCCAACATTTTTTTTTTCT
 TGAGACAGAGTCTTGCTCTGTTGCCAGGCTAGAGTGCAGTGGTGCAATCTCAGTTCACTGC
 AACCTCTGCCTCCCGGGTTCAAGCGATTCTTCTGCCTCAGCCTCCCTAGTGGCTGGGATTAC
 AGGCGCCTGCTACCATGCTGGCTAATTTTTGTATTTTTAGTAGAGATGGGGTTTACCATA
 TTGGCCAGGCTGGTCTTGAACCTCCTGACTTCAGGTGACCCACCCGCTCGGCCTCTCAAAAT
 GCTGGGATTACAGGTGTGAGCCACCGTGCCTGGCCAATTCCAACATTCTTAAATCTCTCAT
 CCCTCCAGGGCTCCCCGTGCTATGTTCTCTTTACCCCTTCCCCCTCTTCTCTTGCTCAGGCC
 TGCACCACTGCAGCCACCGTTCATTTATTTCATTATTAAACACTGAGCACTCACTCTGTGCT
 GGGTCCCGGGAAGGGTGAGGGGGTCAGACACAGGCCCTGCCCTGCCCTCAGTGACTGGCCA
 GTCCAGCCCAGGCGGGGAGAGATGTGTACATAGGTTTTTAAAGCAGACCCAGAGCTCATGGGG
 GCCTGTGTTCTGGGTGTTTCAAGGTGCTGCTGGTCCCTCCATTACCCACTGCTCCCCAAGGCTGG
 TGGGACGGGGTCCCGGTGGCAGGGGCAGGTATCTCCTTCCCGTTCCTCATCCACCTGCCAG
 TGCTCATCGTTACAGCAAACCCAGGGGGCCTTGGCCAGGTCAAGGGTTCTGTGAGGAGAGG
 ACCCAGGAGTGTGGGGGCATTTGGGGGGTGAAGTGGCCCCGGAAGAATGGAACCCACACCCA
 TAGCTCTCCCCACAGCTGATACGGCATCCTGCGAGAAGACCTGCCCTCCTCACTGGGATCCC
 CTTCTGCTCCTCCCAGGGCTCTGCCAGGGCCTTGCTCAGTCCCTTCCACCAAAGTCATCT
 GAACTTCCGTTTCCCCAGGGCTCCAGCTGCCCTCAGACACTGATGTCTGTCCCCAGGTGCT
 CTCTGCCCTCATGCCCTCTCACCGGCCAGTGCCCCGACTCTCCAGGCTTTATCAAGGTG
 AAACACCTGCAGGAGAAGGGCCACGGAAGCCCCAGGCTTTAGAGCCCTCAGCAGGTCTGGGG
 AGCTAGAGCAAAGGAGGGACCTCAGGCCTTCCGTTTCTTCTTCCAGGGTGGGGTGGCCTGGT
 GTTCCCCTAGCCTTCCAAACCCAGGTGGCCTGCCCTTCTCCCCAGAGGGAGGCGGCCTCCGC
 CCATTGGTGCTCATGCAGACTCTGGGGCTGAGGTGCCCGGGGGTGTCTCTGTTGCTCAC
 AGCCGAGGGAGCCGTGGCTCCATGGCCAGATGACGGAAACAGGGTCTGACCAAGTGCCAGGA
 AGACCTGTGCTATAAACACCCCTGCCTGATCCTGCCCTGCCTGACCCCGCCACGCCCTGCC
 GTCCAGCATGATTAAAGAATGCTGTCTCCTCTTGGAATAAAAAAAAAAAAAA

FIGURE 30

MVTAALGPVWAALLLFLLMCEIRMVELTFDRAVASGCQRCCDSEDLDPAHVSSASSSGRPH
ALPEIRPYINITILKGDKGDPGPMGLPGYMGREGPQGEPPGQSGDKGEMGSPGAPCQKRF
FAFSVGRKTALHSGEDFQTLLFERVFVNLDGCFDMATGQFAAPLRGIYFFSLNVHSWNYKET
YVHIMHNQKEAVILYAQPSESRIMQSQSVMLDLAYGDRVWVRLFKRQRENAIYSNDFDTYIT
FSGHLIKAEDD

Important features:

Signal peptide:

amino acids 1-20

N-glycosylation site.

amino acids 72-75

Clq domain proteins.

amino acids 144-178, 78-111 and 84-117

09991111 11111111

FIGURE 31

ACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCCTCGGGCCCGACCCGCCAGGAAAGACTG
 AGGCCGCGGCCTGCCCCGCCCCGGCTCCCTGCGCCGCCGCCCTCCCGGGACAGAAG**ATGTG**
 CTCCAGGGTCCCTCTGCTGCTGCCGCTGCTCCTGCTACTGGCCCTGGGGCTGGGGTGCAGG
 GCTGCCCATCCGGCTGCCAGTGCAGCCAGCCACAGACAGTCTTCTGCACTGCCCCGCCAGGGG
 ACCACGGTGCCCCGAGACGTGCCACCCGACACGGTGGGGCTGTACGTCTTTGAGAACGGCAT
 CACCATGCTCGACGCAGGCAGCTTTGCCGGCCTGCCGGGCTGCAGCTCCTGGACCTGTCAC
 AGAACCAGATCGCCAGCCTGCCAGCGGGGTCTTCCAGCCACTCGCCAACCTCAGCAACCTG
 GACCTGACGGCCAACAGGCTGCATGAAATCACCAATGAGACCTTCCGTGGCCTGCGGCGCCT
 CGAGCGCCTCTACCTGGGCAAGAACCGCATCCGCCACATCCAGCCTGGTGCCTTCGACACGC
 TCGACCGCCTCCTGGAGCTCAAGCTGCAGGACAACGAGCTGCGGGCACTGCCCCCGCTGCGC
 CTGCCCCGCTGCTGCTGCTGGACCTCAGCCACAACAGCCTCCTGGCCCTGGAGCCCGGCAT
 CCTGGACACTGCCAACGTGGAGGCGCTGCGGCTGGCTGGTCTGGGGCTGCAGCAGCTGGACG
 AGGGGCTCTTCAGCCGCTTGCGCAACCTCCACGACCTGGATGTGTCCGACAACAGCTGGAG
 CGAGTGCCACCTGTGATCCGAGGCCTCCGGGGCTGACGCGCCTGCGGCTGGCCGGCAACAC
 CCGCATTGCCAGCTGCGGCCCCGAGGACCTGGCCGGCCTGGCTGCCCTGCAGGAGCTGGATG
 TGAGCAACCTAAGCCTGCAGGCCCTGCCTGGCGACCTCTCGGGCCTCTTCCCCCGCCTGCGG
 CTGCTGGCAGCTGCCCCGAACCCCTTCAACTGCGTGTGCCCCCTGAGCTGGTTTGGCCCCCTG
 GGTGCGCGAGAGCCACGTCACACTGGCCAGCCCTGAGGAGACGCGCTGCCACTTCCCGCCCA
 AGAACGCTGGCCGGCTGCTCCTGGAGCTTGACTACGCCGACTTTGGCTGCCAGCCACCACC
 ACCACAGCCACAGTGCCCAACCAGAGGCCCGTGGTGCGGGAGCCACAGCCTTGTCTTCTAG
 CTTGGCTCCTACCTGGCTTAGCCCCACAGCGCCGGCCACTGAGGCCCCCAGCCCCGCCCTCCA
 CTGCCCCACCGACTGTAGGGCCTGTCCCCCAGCCCCAGGACTGCCACCGTCCACCTGCCTC
 AATGGGGGCACATGCCACCTGGGGACACGGCACCACTGGCGTGCTTGTGCCCCGAAGGCTT
 CACGGGCCTGTACTGTGAGAGCCAGATGGGGCAGGGGACACGGCCCAGCCCTACACCAGTCA
 CGCCGAGGCCACCACGGTCCCTGACCTGGGCATCGAGCCGGTGAGCCCCACCTCCCTGCGC
 GTGGGGCTGCAGCGCTACCTCCAGGGGAGCTCCGTGCAGCTCAGGAGCCTCCGTCTCACCTA
 TCGCAACCTATCGGGCCCTGATAAGCGGCTGGTGACGCTGCGACTGCCTGCCTCGCTCGCTG
 AGTACACGGTCACCCAGCTGCGGCCCAACGCCACTTACTCCGTCTGTGTATGCCTTTGGGG
 CCCGGGCGGGTGCCGGAGGGCGAGGAGGCCTGCGGGGAGGGCCATACACCCCCAGCCGTCCA
 CTCCAACCACGCCCCAGTCACCCAGGCCCGCGAGGGCAACCTGCCGCTCCTCATTGCGCCCCG
 CCCTGGCCGCGGTGCTCCTGGCCGCGCTGGCTGCGGTGGGGGCAGCCTACTGTGTGCGGCGG
 GGGCGGGCCATGGCAGCAGCGGCTCAGGACAAAGGGCAGGTGGGGCCAGGGGCTGGGCCCT
 GGAACCTGGAGGGAGTGAAGGTCCCCTTGAGGCCAGGCCCGAAGGCAACAGAGGGCGGTGGAG
 AGGCCCTGCCAGCGGGTCTGAGTGTGAGGTGCCACTCATGGGCTTCCAGGGCCTGGCCTC
 CAGTCACCCCTCCACGCAAAGCCCTACATC**TAA**GCCAGAGAGAGACAGGGCAGCTGGGGCCG
 GGCTCTCAGCCAGTGAGATGGCCAGCCCCCTCCTGCTGCCACACCACGTAAGTTCTCAGTCC
 CAACCTCGGGGATGTGTGCAGACAGGGCTGTGTGACCACAGCTGGGCCCTGTTCCCTCTGGA
 CCTCGGTCTCCTCATCTGTGAGATGCTGTGGCCAGCTGACGAGCCCTAACGTCCCCAGAAC
 CGAGTGCCATATGAGGACAGTGTCCGCCCTGCCCTCCGCAACGTGCAGTCCCTGGGCACGGCG
 GGCCCTGCCATGTGCTGGTAACGCATGCCTGGGTCTGCTGGGCTCTCCCACTCCAGGCGGA
 CCCTGGGGGCCAGTGAAGGAAGCTCCCGGAAAGAGCAGAGGGAGAGCGGGTAGGCGGCTGTG
 TGA CTCTAGTCTTGGCCCCAGGAAGCGAAGGAACAAAAGAACTGGAAAGGAAGATGCTTTA
 GGAACATGTTTTGCTTTTTTAAATATATATATTTATAAGAGATCCTTTCCCATTTATTCTG
 GGAAGATGTTTTTCAAACCTCAGAGACAAGGACTTTGGTTTTTGTAAAGACAAACGATGATATG
 AAGGCCTTTTGTAAAGAAAAATAAAAGATGAAGTGTGAAA

FIGURE 32

MCSRVP LLLPL LLLL LALGPGVQGCPSGCQCSQPQTVFCTARQGTTVPRDVPPDTVGLYVFEN
GITMLDAGSFAGLPGLQLLDLSQNQIASLPSGVFQPLANLSNLDLTANRLHEITNETFRGLR
RLERLYLGKNRIRHIQPGAFDTLDRLLELKLQDNELRALPPLRLPRLLLLDLSHNSLLALEP
GILDTANVEALRLAGLGLQQLDEGLFSRLRNLDLDVSDNQLERVPPVIRGLRGLTRLRLAG
NTRIAQLRPEDLAGLAALQELDVSNSLSLQALPGDLSGLFPRLRLLAAARNPFNCVCPLSWFG
PWVRESHVTLASPEETRCHFPKNAGRLLLELDYADFGCPATTTTATVPTTRPVVREPTALS
SSLAPTWLSPTAPATEAPSPPSTAPPTVGPVPQPQDCPPSTCLNGGTCHLGTRHHLACLCPE
GFTGLYCESQMGQGTRPSPTPVTPRPPRSLTLGIEPVSPSLRVGLQRYLQGSSVQLRSLRL
TYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSVCVMPLGPGRVPEGEEACGEAHTPPA
VHSNHAPVTQAREGNPLLIAPALAAVLLAALAAVGAAYCVRGRAMAAAAQDKGQVGPAG
PLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPGLQSPHAKPYI

TQSTT "TBT66D

FIGURE 33

GAATCATCCACGCACCTGCAGCTCTGCTGAGAGAGTGCAAGCCGTGGGGGTTTTGAGCTCAT
 CTTTCATCATTCATATGAGGAAATAAGTGGTAAATCCTTGAAATACA**ATG**GAGACTCATCAG
 AAACATTTACATATTTTGTAGTATTGTTATGACAGCAGAGGGTGATGCTCCAGAGCTGCCAG
 AAGAAAGGGAACTGATGACCAACTGCTCCAACATGTCTCTAAGAAAGGTTCCCGCAGACTTG
 ACCCCAGCCACAACGACACTGGATTTATCCTATAACCTCCTTTTTCAACTCCAGAGTTCAGA
 TTTTCATTCTGTCTCCAAACTGAGAGTTTTGATTCTATGCCATAACAGAATTC AACAGCTGG
 ATCTCAAAACCTTTGAATTCACAAGGAGTTAAGATATTTAGATTTGTCTAATAACAGACTG
 AAGAGTGTAACCTTGGTATTTACTGGCAGGTCTCAGGTATTTAGATCTTTCTTTTAATGACTT
 TGACACCATGCTATCTGTGAGGAAGCTGGCAACATGTCACACCTGGAAATCCTAGGTTTGA
 GTGGGGCAAAAATACAAAATCAGATTTCCAGAAAATTGCTCATCTGCATCTAAATACTGTC
 TTCTTAGGATTGAGAACTCTTCCTCATTATGAAGAAGGTAGCCTGCCCATCTTAAACACAAC
 AAAACTGCACATTGTTTTACCAATGGACACAAATTTCTGGGTTCTTTGCGTGATGGAATCA
 AGACTTCAAAAATATTAGAAATGACAAATATAGATGGCAAAAGCCAAATTTGTAAGTTATGAA
 ATGCAACGAAATCTTAGTTTTAGAAAATGCTAAGACATCGGTTCTATTGCTTAATAAAGTTGA
 TTTACTCTGGGACGACCTTTTCCTTATCTTACAATTTGTTTGGCATAACATCAGTGGAACACT
 TTCAGATCCGAAATGTGACTTTTGGTGGTAAGGCTTATCTTGACCACAATTCATTTGACTAC
 TCAAATACTGTAATGAGAACTATAAAATGGAGCATGTACATTTAGAGTGTTTTACATTTCA
 ACAGGATAAAATCTATTTGCTTTTGACCAAAATGGACATAGAAAACCTGACAATATCAAATG
 CACAAATGCCACATGCTTTTCCCGAATTATCCTACGAAATTCGAATATTTAAATTTTGCC
 AATAATATCTTAACAGACGAGTTGTTTTAAAGAAGTATCCAACCTGCCTCACTTGAAAACCTCT
 CATTTTGAATGGCAATAAACTGGAGACACTTTCTTTAGTAAGTTGCTTTGCTAACAACACAC
 CTTTGGAACTTGGATCTGAGTCAAAATCTATTACAACATAAAAATGATGAAAATTTGCTCA
 TGGCCAGAAACTGTGGTCAATATGAATCTGTCTATACAATAAATTTGTCTGATTCTGTCTCAG
 GTGCTTGCCCAAAAGTATTCAAATACTTGACCTAAATAATAACCAATCCAACTGTACCTA
 AAGAGACTATTCATCTGATGGCCTTACGAGAAGTAAATATTGCATTTAATTTTCTAACTGAT
 CTCCCTGGATGCAGTCATTTAGTAGACTTTAGTTCTGAACATTTGAAATGAACCTTCATTCT
 CAGCCCATCTCTGGATTTTGTTCAGAGCTGCCAGGAAGTTAAACTCTAAATGCGGGAAGAA
 ATCCATTCGGGTGATACCTGTGAATTTAAATAAATTTTATTGAGCTTGAACATATTAGAGGTC
 ATGATGGTTGGATGGTCAGATTCATACACCTGTGAATACCCTTTAAACCTAAGGGGAAGTAG
 GTTAAAGACGTTTCATCTCCACGAATTATCTTGCAACACAGCTCTGTTGATTGTCACCATTG
 TGGTTATTATGCTAGTTCTGGGGTTGGCTGTGGCCTTCTGCTGTCTCCACTTTGATCTGCCC
 TGGTATCTCAGGATGCTAGGTCAATGCACACAAACATGGCACAGGGTTAGGAAAACAACCCA
 AGAACAAGTCAAGAGAAATGTCCGATTCCACGCATTTATTTTATACAGTGAAACATGATTCTC
 TGTGGGTGAAGAATGAATTGATCCCCAATCTAGAGAAGGAAGATGGTTCTATCTTGATTTCG
 CTTTATGAAAGCTACTTTGACCCTGGCAAAAGCATTAGTGAAAATATTGTAAGCTTCATTGA
 GAAAAGCTATAAGTCCATCTTTGTTTTGTCTCCCAACTTTGTCCAGAATGAGTGGTGCCATT
 ATGAATTTCTACTTTGCCCAACCAATCTCTCCATGAAAATTTCTGATCATATAATTCTTATC
 TTACTGGAACCCATTCCATTCTATTGCAATTTCCCAAGGTATCATAAACTGAAAAGCTCTCCT
 GGAAAAAAGCATACTTGGAAATGGCCCAAGGATAGGCGTAAATGTGGGCTTTTCTGGGCAA
 ACCTTCGAGCTGCTATTAATGTTAATGTATTAGCCACCAGAGAAATGTATGAACTGCAGACA
 TTCACAGAGTTAAATGAAGAGTCTCGAGGTTCTACAATCTCTCTGATGAGAACAGATTGTCT
ATAAAATCCCACAGTCTTGGGAAGTTGGGGACCACATACACTGTTGGGATGTACATTGATA
 CAACCTTTATGATGGCAATTTGACAATATTTATTTAAATAAAAAATGGTTATTCCCTTCATA
 TCAGTTTCTAGAAGGATTTCTAAGAATGTATCCTATAGAAACACCTTCACAAGTTTATAAGG
 GCTTATGGAAAAAGGTGTTTCATCCCAGGATTGTTTTATAATCATGAAAAATGTGGCCAGGTGC
 AGTGGCTCACTCTTGTAATCCCAGCACTATGGGAGGCCAAGGTGGGTGACCCACGAGGTCAA
 GAGATGGAGACCATCCTGGCCAACATGGTGAACCTGTCTCTACTAAAAATACAAAATTA
 GCTGGGCGTGATGGTGCACGCCTGTAGTCCCAGCTACTTGGGAGGCTGAGGCAGGAGAATCG
 CTTGAACCCGGGAGGTGGCAGTTGCAGTGAGCTGAGATCGAGCCACTGCACTCCAGCCTGGT
 GACAGAGCGAGACTCCATCTCAAAAAAAGAAAAAAGAAAAAATGGAAAAACATCC
 TCATGGCCACAAAATAAGGTCTAATTCATAAATTATAGTACATTAATGTAATATAATATTA
 CATGCCACTAAAAAGAATAAGGTAGCTGTATTTCTGGTATGGAAAAACATATTAATAT
 GTTATAAACTATTAGGTTGGTGCAAAATCAATTTGTGGTTTTTGGCATTGAAATGGCATTGAA
 ATAAAAGTGTAAGAAATCTATACCAGATGTAGTAACAGTGGTTTGGGTCTGGGAGGTGGA
 TTACAGGGAGCATTTGATTTCTATGTTGTGTATTTCTATAATGTTTGAATTTGTTTAGAATGA
 ATCTGTATTTCTTTTATAAGTAGAAAAAATAAAGATAGTTTTTACAGCCT

FIGURE 34

MRLIRNIYIFCSIVMTAEGDAPELPEERELMTNCSNMSLRKVPADLTPATTTLDLSYNLLFQ
LQSSDFHSVSKLRVLILCHNRIQQDLKTFFFNKELRYLDLSNNRLKSVTWYLLAGLRYLDL
SFNDFDTMPICEEAGNMSHLEILGLSGAKIQKSDFQKIAHLHLNTVFLGFRTLPHYEEGSLP
ILNTTKLHIVLPMDTNFWVLLRDGIKTSKILEMTNIDGKSQFVSYEMQRNLSLENAKTSVLL
LNKVDLLWDDLFLILQFVWHTSVEHFQIRNVTFGGKAYLDHNSFDYSNTVMRTIKLEHVHFR
VFYIQQDKIYLLLTkMDIENLTISNAQMPHMLFPNYPTKFQYLNFANNILTDELFKRTIQLP
HLKTLILNGNKLETLSLVSCFANNTPLEHLDLSQNLLQHKNDENC SWPETVVNMNLSYNKLS
DSVFRCLPKSIQILD LNNNQIQTVPKETIHLMALRELNIAFNFLTDLPGC SHFSRLSVLNIE
MNFILSPSLDFVQSCQEVKTLNAGRNPFRCTCELKNFIQLETYSEVMMVGWSDSYTCEYPLN
LRGTRLKDVHLHELSCNTALLIVTIVVIMLVGLAVAFCC LHFDLPWYLRMLGQCTQTWHRV
RKTTQEQLKRNVRFHAFISYSEHDSLWVKNELIPNLEKEDGSILICLYESYFDPGKSISENI
VSFIEKSYKSIFVLSPNFVQNEWCHYEFYFAHHNLFHENS DHIILILLEPIPFYCIPTRYHK
LKALLEKKAYLEWPKDRRCGLFWANLRAAINVNVLATREMYELQTFTELNEESRGSTISLM
RTDCL

F09T "T3T650

GGGGGCTTTCTTGGGCTTGGCTGCTTGGAAACACCTGCCTCCAAGGACCGGCCCTCGGAGGGGTGCCGGGAAAGG
GAGGGAAGAAAGGAAGGGCGGGGCGCCCGCTGCGCCCGCCCGCGCCTCTGCGCGCCCTGTCCGCCCCGGC
CCAGCCCAGCCCAGCCCCGCGGGCCGGTACACGCGCAGCCAGCCGCGCCCTCCCGCGCCCAAGCGCGCCGCT
CTGCTGTGCCCTGCGCCCTTGGCCCGCGCCAGCTTCTGCGCCCGCAGCCCGCCCGGCGCCCCCGGTGACCGTGA
CCCTGCCCTGGGCGCGGGGCGGAGCAGGCATGTCCTCCCGCCCGGGGACCGCTACCCAGCGCTGGCCCTGGTGCTC
CTGGCAGTGACCTTGGCCGGGGTTCGGAGCCAGGGCGCAGCCCTCGAGGACCTGATTATTACGGGAGGAGAT
CTGGAGCCGGGAGCCCTACTACGCGCGCCCGAGCCCGAGCTCGAGACCTTCTCTCCGCGCTGCCTGCGGGGGC
CCGGGGAGGAGTGGGAGCGCGCCCGCAGGAGCCAGGCCGCCCAAGAGGGCCACCAAGCCCAAGAAAGCTCCC
AAGAGGGAGAAGTCCGGTCCGGAGCCGCTCCACCAGGTAACACAGCAACAAAAAGTTATGAGAACCAAGAG
CTCTGAGAAGGCTGCCAACGATGATCACAGTGTCCGTGTGGCCCGTGAAGATGTGAGAGAGAGTTGCCACCTC
TTGGTCTGGAAACCTTAAAAATCACAGACTTCCAGCTCCATGCCTCCACGGTGAAGCGCTATGGCCTGGGGGCA
CATCGAGGGAGACTCAACATCCAGGCGGGCATTAATGAAATGATTTTTATGACGGAGCGTGGTGCGCGGGAAG
AAATGACCTCCAGCAGTGGATTGAAGTGGATGCTCGGCCCTGACGAGATTACTGGTGTCTACTCAAGGGA
GGAACCTCCCTCTGGCTGAGTGACTGGGTGACATCCTATAAGGTCATGGTGAGCAATGACAGCCACACGTGGGT
ACTGTTAAGAATGGATCTGGAGACATGATATTTGAGGGAAACAGTGAGAAGGAGATCCCTGTTCTCAATGAGCT
ACCCGTCCCCATGGTGGCCCGCTACATCCGCATAAACCTCAGTCTGTTTGATAATGGGAGCATCTGCATGA
GAATGGAGATCCTGGGCTGCCACTGCCAGATCCTAATAATTATTATCACCGCCGGAACGAGATGACCCACT
GATGACCTGGATTTTTAAGCACCACAATTATAAGGAATGCGCCAGTTGATGAAAGTTGTGAATGAAATGTGTCC
CAATATCACCAGAAATTTACAACATTGGAAAAAGCCACGAGGCCCTGAAGCTGTATGCTGTGGAGATCTCAGATC
ACCTTGGGAGCATGAAGTCGGTGAGCCGAGTTCACCTACATCGCGGGGGCCACGGCAATGAGGTGCTGGGC
CGGGAGCTGCTGCTGCTGCTGGTGCAGTTCGTGTGTGAGGAGTACTTGGCCCGGAATGCGCGCATCGTCCACCT
GGTGGAGGAGACGCGGATTACGTCCTCCCTCCCTCAACCCCGATGGCTACGAGAAGGCCCTACGAAGGGGGCT
CGGAGCTGGGAGGCTGGTCCCTGGGACGCTGGACCCACGATGGAATTGACATCAACAACAACCTTCTGATTTA
AACACGCTGCTCTGGGAGGAGAGGATCGACGAAATGTCCCCAGGAAGGTTCCCAATCACTATATGCAATCCC
TGAGTGGTTTCTGTGCGAAAATGCCAGCGTGGCTGCCAGCAGAGAGTTCATAGCTGGATGGAAAAAATCC
CTTTTGTGCTGGGCGGCAACCTGCAAGGCGGCGAGCTGGTGGTGGCGTATCCCTACGACCTGGTGGGTCCCC
TGGAAGACGCGAGGAACACACCCCCACCCCGATGACCACGTGTTCCGCTGGCTGGCTACTCCTATGCCTCCAC
ACACCGCCTCATGACAGACGCCCCGAGGAGGGTGTGCCACACGGAGGACTTCCAGAAGGAGGAGGGCAGTGTCA
ATGGGGCCTCCTGGCACACCGTCGCTGGAAGTCTGAACGATTTTCAGTACCTTATACAAACTGCTTCGAATG
TCCATCTACGTGGGCTGTGATAAATACCCACATGAGAGCCAGCTGCCCGAGGAGTGGGAGGAATAACCGGAATC
TCTGATCGTGTTTCATGGAGCAGGTTATCGTGGCATTAAGGCTTGGTGAGAGATTACATGGAAAAGGAATCC
CAAACGCCATTTATCTCCGTAGAAGGCATTAACCATGACATCCGAACAGCCAACGATGGGGATTACTGGCGCCTC
CTGAACCCCTGGAGAGTATGTGGTCACAGCAAAGGCCGAAGGTTTCACTGCATCCACCAAGAACTGTATGGTTGG
CTATGACATGGGGGCCACAAGGTGTGACTTCACACTTAGCAAAACCAACATGGCCAGGATCCGAGAGATCATGG
AGAAGTTTGGGAAGCAGCCCGTCAGCCTGCCAGCCAGGCGGCTGAAGCTGCGGGGGCGGAAGAGACGACGCT
GGGTGAACCCCTCCTGGGCGCTTGAAGATCGTCTGGGACCCATGCAAAATTAACCAACCTGGTAGTAGCTCCATAG
TGGACTCACTCACTGTTGTTTCTCTGTAATCAAGAAGTGCTTGAAGAGAGGGTGCATTGTGAGGCAGGTCC
CAAAAGGGAAGGTGAGGCTGAGGCTGAGGCTGTTTTCTTTTCTTTGTTCCCATTTATCCAAATAACTTGGACAGAGCA
GCAGAGAAAAGCTGATGGGAGTGAGAGAACTCAGCAAGCCAACCTGGGAATCAGAGAGAGAAGGAGAAGGAGGG
GAGCCTGTCCGTTTCAGAGCCTCTGGCTGCATAGAAAAGGATTCTGGTGCTTCCCCTGTTTGGCTGGCAGCAAGG
GTTCCACGTGCATTTGCAATTTGCACAGCTAAAATTGCAGCATTTCCCAGCTGGGCTGTCCCAAGTGTATACCA
TTTGAGATGCTCCCAGGCGTCTTAAGAGAATCCACCTCTCTGGCCCTGGGACATTGCAAGCTGACATCAAAATA
ATTCTGTGTTCTTTGACAATAGCGTATTGGCAAGTGACATCAGTGAAGCCTTGAATCTGTTTGTGCTCTCT
TTTTCAACAAGAGAGTGTTTCAGAAAAGGAGAGAGAGGCTGAGATCATTCAGGAGTTTGTGGGCAGCAAGCA
TGGAGCTTCTTGCACAAATTTCTGGGTCCATAAACAAACCCCAAGTCCCTGCTGATCCAGTAGCCCTGGAGGTT
CCCCAGGTAGGGAGAGCCAGAGTGCCAGCCTTCTTGAAGGGCCAGAAAATTTAGCCTGGATCTCCTCTTTTAC
CTGCTAGGACTGGAAAGAGCCAGAAGTGGGGTGGCCTGAAGCCCTCTCTGCTTGGAGTATTGCCCTGTGTG
GAATTGAGTGCTCATGGGTGGCCCTCATATCAGCCTGGGAGTTATTTTTGATATGATAATGCCAGATCTTCCA
GATTAGGCTAAATGTAATGAAACCTCTTAGGATTTATCTGTGGAGCATCAGTTTGGGAAGAATTATTGAATTAT
CTTGGCAAGAAAAAGATGTGCTCACTTTTGTGTTAATGTTGTGCTGCCTCATTGACCTGGGAAAAATGAAAAAAA
AATAAAGCAAATGGTAAGACCCTTAAA

FIGURE 36

MSRPGTATPALALVLLAVTLAGVGAQGALEDPDYYGQEIWSREPYARPEPELETFSPPLP
AGPGEEWERRPQEPRPPKRATKPKKAPKREKSAPEPPPPGKHSNKKVMRTKSSEKAANDDHS
VRVAREDVRESCPPLGLETLKITDFQLHASTVKRYGLGAHRGRLNIQAGINENDFYDGAWCA
GRNDLQQWIEVDARRLTRFTGVITQGRNSLWLSDWVTSYKVMVSNDSTWVTVKNGSGDMIF
EGNSEKEIPVLNELPVPMPVARYIRINPQSWFDNGSICMRMEILGCPLPDPNNYYHRRNEMTT
TDDLDFKHHNYKEMRQLMKVVNEMCPNITRIYNIGKSHQGLKLYAVEISDHPGEHEVGEPEF
HYIAGAHGNEVLGRELLLLLVQFVCQEYLARNARIVHLVEETRIHVLPSLNPDGYEKAYEGG
SELGGWSLGRWTHDGIDINNNFPDLNTLLWEAEDRQNVPRKVPNHYYIAIPEWFLENATVAA
ETRAVIAWMEKIPFVLGGNLQGGELVVAYPYDLVRSPWKTQEHTPTPDDHVFRWLAYSAST
HRLMTDARRRVCHTEDFQKEEGTVNGASWHTVAGSLNDFSYLHTNCFELSIYVGCDKYPHES
QLPEEWENNRESLIVFMEQVHRGIKGLVRDSHGKIPNAIISVEGINHDIRTANDGDYWRL
NPGEYVVTAKAEGFTASTKNCMVGYDMGATRCDFTLSTKNMARIREIMEKFGKQPVSLPARR
LKLGRGRRRQRG

CTAAGAGGACAAGATGATGAGGCCCGGCTCTCATTTCTCCTAGCCCTTCTGTTCCTTGGCCAAGCTGCAGGGG
ATTTGGGGGATGTGGGACCTCCAATTCCCAGCCCCGGCTTCAGCTCTTTCCCAGGTGTTGACTCCAGCTCCAGC
TTCAGCTCCAGCTCCAGGTCCGGGCTCCAGCTCCAGCCGACGCTTAGGCAGCGGAGGTTCTGTGTCCCAGTTGTT
TTCCAAATTTACCCGGCTCCGTGGATGACCGTGGGACCTGCCAGTGCTCTGTTTCCCTGCCAGACACCACCTTTT
CCGTGGACAGAGTGAACGCTTGAATTCACAGCTCATGTTCTTTCTCAGAAGTTTGAGAAAGAAGCTTTCTAAA
GTGAGGGAATATGTCCAATTAATTAGTGTGTATGAAAAGAACTGTTAAACCTAACTGTCCGAATTGACATCAT
GGAGAAGGATACCATTCTTACACTGAACTGGACTTCGAGCTGATCAAGGTAGAAGTGAAGGAGATGGAAAAA
TGGTCATACAGCTGAAGGAGAGTTTTGGTGAAGCTCAGAAATTGTTGACCAGCTGGAGGTGGAGATAAGAAAT
ATGACTCTCTTGGTAGAGAAAGCTTGAGACACTAGACAAAAACAATGTCCCTGGCCATTCGCCAGAAAATCGTGGG
TCTGAAGACCAAGCTGAAAGAGTGTGAGGCCTCTAAAGATCAAAACACCCCTGTCTGCCACCTCTCCCCTAA
CAGGGAGCTGTGGTCATGGTGGTGTGGTGAACATCAGCAAAACCGTCTGTGGTTCAGCTCAACTGGAGAGGGTTT
TCTTATCTATATGGTGCTTGGGGTAGGGATTACTCTCCCAGCATCCAAACAAGGACTGTATTGGGTGGCGCC
ATTGAATACAGATGGGAGACTGTTGGAGTATTATAGACTGTACAACACACTGGATGATTTGCTATTGTATATAA
ATGCTCGAGAGTTGCGGATCACCTATGGCCAAGGTAGTGGTACAGCAGTTTACAACAACAACATGTACGTCAC
ATGTACAACACCCGGGAATATTGCCAGAGTTAACTTGACCACCAACACGATTGCTGTGACTCAAATCTCCCCTAA
TGCTGCCTATAATAACCGCTTTTCATATGCTAATGTTGCTTGGCAAGATATTGACTTTGCTGTGGATGAGAAT
GATTGTGGGTTATTATTCAACTGAAGCCAGCACTGGTAACATGGTGATTAGTAACTCAATGACACCACACTT
CAGGTGCTAAACACTTGGTATACCAAGCAGTATAAACCATCTGCTTCTAACGCCTTCATGGTATGTGGGGTTCT
GTATGCCACCCGTACTATGAACACCAGAACAGAAGAGATTTTTTACTATTATGACACAAACACAGGGAAAGAG
GCAAACTAGACATTGTAATGCATAAGATGCAGGAAAAAGTGCAGAGCATTAACTATAACCCCTTTTGACCAGAAA
CTTTATGTCTATAACGATGGTTACCTTCTGAATTATGATCTTTCTGTCTTGCAAGCCCCAGCTAAAGCTGTTTA
GGAGTTAGGTTGAAAGAGAAAAATTTGTGTAAAAAATAGTCTTCCACTTACTTAGATATGCGAGGGGTGT
CTAAAAGTGTGTTTCATTTTGCGAGCAATGTTTAGGTGCATAGTTCTACCACACTAGAGATCTAGGACATTTGTCT
TGATTTGGTGAGTTCTCTTGGGAATCATCTGCCTCTTCAGGCGCATTTTGCAATAAAGTCTGTCTAGGGTGGGA
TTGTCAAGGTCTAGGGGCACCTGTGGGCCTAGTGAAGCCTACTGTGAGGAGGCTTCACTAGAAGCCTTAAATTA
GGAATTAAGGAACTTAAAACTCAGTATGGCGTCTAGGGATTCTTTGTACGAGAAATATTGCCCAATGACATAGTC
CTCATCCATGTAGCACCCTAATCTTCCATGCCTGGAAGAAACCTGGGACTTAGTTAGGTAGATTAATATCT
GGAGCTCTCGAGGGACCAAACTCCAACCTTTTTTTTCCCCCTACTAGCACCTGGAATGATGCTTTGTATGTGG
CAGATAAGTAAATTTGGCATGCTTATATATTCTACATCTGTAAAGTGCTGAGTTTTATGGAGAGAGGCCCTTTTT
ATGCATTAAATTGTACATGGCAAATAAATCCAGAAGGATCTGTAGATGAGGCACCTGCTTTTTCTTTTCTCTC
ATTGTCCACCTTACTAAAAGTCAGTAGAATCTTCTACCTCATAACTTCCTTCCAAAGGCAGCTCAGAAGATTAG
AACAGACTTACTAACCAATTCACCCCCCAACCAACCCCTTCTACTGCCTACTTTAAAAAATTAATAGTTTTT
CTATGGAACTGATCTAAGATTAGAAAAATTAATTTCTTTAATTTCAATTAGGACTTTTTATTACATGACTCTA
AGACTATAAGAAAACTGATGGCAGTGACAAAGTGCTAGCATTTATTGTTATCTAATAAAGACCTTGGAGCATA
TGTGCAACTTATGAGTGTATCAGTTGTTGCATGTAATTTTTGCCTTTGTTTAAGCCTGGAAGTGTGAAGAAAT
GAAAATTTAATTTTTTTTTTCTAGGACGAGCTATAGAAAAGCTATTGAGAGTATCTAGTTAATCAGTGCAGTAGT
TGGAAACCTTGCTGGTGTATGTGATGTGCTTCTGTGCTTTTGAATGACTTTATCATCTAGTCTTTGTCTATTTT
TCCTTTGATGTTCAAGTCTAGTCTATAGGATTGGCAGTTTGAATGCTTTACTCCCCCTTTTAAATAAATGAT
TAAATGTGCTTTTAAAAAATAAAAAAAAAAAAAAAAAAAAAA

FIGURE 38

MRPGLSFLLALLFFLGQAAGDLGDVGPPIPSPGFSSFPBGVDSSSSFSSSSSRSGSSSSSRSLGS
GGSVSQLFSNFTGSVDDRGTCQCSVSLPDTTFPVDRVERLEFTAHVLSQKFEKELSKVREYV
QLISVYEKLLNLTVRIDIMEKDTISYTELDFELIKVEVKEMEKLVIQLKESFGGSSEIVDQ
LEVEIRNMTLLVEKLETLDKNNVLAIRREIVALKTKLKECEASKDQNTPVVHPPPTPGSCGH
GGVVNISKPSVVQLNWRGFSYLYGAWGRDYSPQHNPNGLYWVAPLNTDGRLLLEYRLYNTLD
DLLLYINARELRITYGQSGTAVYNNNMYVNMNTGNIARVNLTNTIAVTQTLNAAAYNNR
FSYANVAWQDIDFAVDENGLWVIYSTEASTGNMVISKLNDTTLQVLNTWYTKQYKPSASNAF
MVCGLYATRTMNRTEEIFYYYDTNTGKEGKLIVMHKMQEKVQSINYNPFDQKLYVYNDG
YLLNYDLSVLQKPQ

FIGURE 39

GCTCTGAAGACCAAGCTGAAAGAGTGTGAGGCCTCTAAAGATCAAACACCCCTGTCGTCCAC
CCTCCTCCCACTCCAGGGAGCTGTGGTCATGGTGGTGTGGTGAACATCAGCAAACCGTCTGT
GGTTCAGCTCAACTGGAGAGGGTTTTCTTATCTATATGGTGCTTGGGGTAGGGATTACTCTC
CCCAGCATCCAAACAAAGGNATGTATTGGGNGGCGCCATTGAATACAGATGGGAGACTGTTG
GAGTATTATAGACTGTACAACCCACTGGATGATTTGCTATTGTATATAAATGCTCGAGAGTT
GCGGATCACCTATGGCCAAGGTAGTGGTACAGCAGTTTACAACAACAACATGTACGTCAACA
TGTACAACACCGGNATATTGCCAGAGTTAACCTGACC

TCTCGCAGATAGTAAATAATCTCGGAAAGGCGAGAAAGAAGCTGTCTCCATCTTGTCTGTAT
CCGCTGCTCTTGTGACGTTGTGGAGATCGGGGAGCGTCCTGGGGCTGTGCTCCATGGCGAGCT
GGATAACCATGTTTGTGTGGAAGTGCCCCGTGTTTGCTATGCCGATGCTGTCTAGTGGAAAC
AACTCCACTGTAACTAGATTGATCTATGCACCTTTTCTTGCTTGGTGGAGTATGTGTAGCTTG
TGTAATGTTGATACCGGAATGGAAGAACAACTGAATAAGATTCTCGGATTTTGTGAGAATG
AGAAAGGTGTTGTCCCTGTGAACATTTTGGTTGGCTATAAAGCTGTATATCGTTTGTGCTTT
GGTTTGGCTATGTTCTATCTTCTTCTCTCTTTACTAATGATCAAAGTGAAGAGTAGCAGTGA
TCCTAGAGCTGCAGTGCACAATGGATTTTGGTTCTTTAAATTTGCTGCAGCAATTGCAATTA
TTATTGGGGCATTCTTTCATTCAGGAAGGAACTTTTACAACCTGTGTGGTTTTATGTAGGCATG
GCAGGTGCCTTTTGTTCATCCATCAGCACTAGTCTTACTTATGATTTTGCACATTTCATG
GAATGAATCGTGGGTTGAAAAAATGGAAGAAGGGAACTCGAGATGTTGGTATGCAGCCTTGT
TATCAGCTACAGCTCTGAATTATCTGCTGTCTTTAGTTGCTATCGTCCTGTTCTTTGTCTAC
TACACTCATCCAGCCAGTTGTTTACAGAAAACAAGGCGTTCATCAGTGTCAACATGCTCCTCTG
CGTTGGTGCTTCTGTAATGTCTATACTGCCAAAAATCCAAGAATCACAACCAAGATCTGGT
TGTTACAGTCTTTCAGTAATTACAGTCTACACAATGTATTTGACATGGTCAGCTATGACCAAT
GAACCAGAAACAAATTGCAACCCCAAGTCTACTAAGCATAAATGGCTACAATACAACAAGCAC
TGTCCTCCAAAGGAAGGGCAGTCCAGTCCAGTGGTGGCATGCTCAAGGAATTATAGGACTAATTC
TCTTTTTTGTGTGTGTATTTTATTCCAGCATCCGTACTTCAAACAATAGTCAGGTTAATAAA
CTGACTCTAACAAGTGATGAATCTACATTAATAGAAGATGGTGGAGCTAGAAGTGATGGATC
ACTGGAGGATGGGGACGATGTTTCCAGGAGCTGTAGATAATGAAAGGGATGGTGTCACTTACA
GTTATTTCTTCTTCACTTCACTGCTTTTTCTGGCTTCACTTTATATCATGATGACCCTTACC
AACTGGTCCAGTATGAACCCTCTCGTGAGATGAAAAGTCAGTGGACAGCTGTCTGGGTGAA
AATCTCTTCCAGTTGGATTGGCATCGTGCTGTATGTTTGGACACTCGTGGCACCACCTTGTTC
TTACAAATCGTGATTTTGACTGAGTGAGACTTCTAGCATGAAAGTCCCACCTTTCATTATTGC
TTATTTGAAAACAGTATTCCCAACTTTTGTAAAGTTGTGTATGTTTTGCTTCCCATGTAAC
TTCTCCAGTGTTCTGGCATTCGAATTAGATTTTACTGCTTGTCTATTTTGTATTTTTCTTACCAA
TGTGATTGATATGTGAAGTAGAATGAATTGCAGAGGAAAGTTTTATGAATATGGTGATGAGT
TAGTAAAAGTGGCCATTATTGGGCTTATTCTCTGCTCTATAGTTGTGAAATGAAGAGTAAAA
ACAAATTTGTTTGACTATTTTAAATTTATATTAGACCTTAAGCTGTTTTCAGCAAGCATAAA
GCAAAATGTATGGCTGCCTTTTGAAATATTTGATGTGTTGCCTGGCAGGATACTGCCAAGAAC
ATGGTTTTATTTTAAATTTTATAACAAGTCACTTAAATGCCAGTTGTCTGAAAAATCTTATA
AGGTTTTTACCCTTGATACGGAATTTACACAGGTAGGGAGTGTTTAGTGGACAATAGTGTAGG
TTATGGATGGAGGTGTGCGTACTAAATTGAATAACGAGTAAATAATCTTACTTGGGTAGAGA
TGGCCTTTGCCAACAAAGTGAACCTGTTTTGGTTGTTTTAACTCATGAAGTATGGGTTAGT
GGAATGTTTGAACCTCTGAAGGATTTAGACAAGGTTTTGAAAAGGATAATCATGGGTTAGA
AGGAAGTGTTTTGAAAGTCACTTTGAAAGTTAGTTTTGGGCCCAGCACGGTAGCTCACCTT
GGTAATCCCAGCACTTTGGGAGCTTAAAGTGGGTAGATTACTTGAGCCCAGGAATTCAGACCA
GCTTGGCACATGGTGAACCTGTTCTATAAAAAATAATCTGGCTTTGAGCATATGCCTGTGGTC
CAGCACTGAGAGGCTAGTGAAGATTGCTGAGCCCAAGCCAAAGGTTGCAGTGAGCAAGTCA
CGTCACTGCACTCTAGCTGGCAGCAGAGTAGGCCAAAAAATATATATATTGAAATCAAGG
AGGCAAAATTTGACAGGGAAGGAAGTAACTGCAAAACCACTAGGCTTTAGTAGGTACTTAT
ATAAAATCTAGTCCAGTTCTCTCATTTAAAAAAATGAAGACACTGAAATACAGACTTAAATA
GCTCAGATAGCTAATTAGGAAATTTCAAGTTGGCCAATAATAGCATTCTCTCGACATTTAA
AAATAATTTCTATTTCAAAATACATGCATATTGATTTACACCTCATACTGTGATAATTAATGT
GATGTGGATTGCTGGTGTCCAGCATGAGCCATAAACAGGTGAGAAGAATGATGGAATGTTTT
AGAATAAACTCCTGCTTATAGTATACTACACAGTTCAAAGATGTTTAAATGCTTTTGTAT
TTACTGCCATGTAATTGAAATATATAGATTATTGTAACCTTTCAACCTGAAAATCAAGCAGT
ATGAGAGTTTTAGTTATTTGTATGTGTCACTAGTGTCTAATGAAGCTTTTAAATCTACAATT
TCTTCTTTAAAAATATTTATTAATGTGAATGGAATATAACAATTCAGCTTAATTTCCCCAAC
TTATTCGTGTGTAGACATTGATTCCACAATTTTGAATGGCTGTGTTTTACCTCTAAATAA
ATGAATTCAGAGAAAAA

MGSVLGLCSMASWIPCLCGSAPCLLCRCCPSGNNSTVTRLIYALFLLVGVCVACVMLIPGME
EQLNKIPGFCENEKGVVPCNIIVGKYKAVYRLCFGLAMFYLLLSLLMIKVKSSSDPRAAVHNG
FWFFKFAAAIAIIIGAFFIPEGFTTTVWFYVGMAGAFCFILIQLVLLIDFAHSWNESWVEKM
EEGNSRCWYAALLSATALNYLLSLVAIVLFFVYYTHPASCSENKAFISVNMLLCVGASVMSI
LPKIQESQPRSGLLQSSVITVYTMYLTSAMTNEPETNCNPSSLISIIGYNTTSTVPKEGQSV
QWWHAQGIIGLILFLLCVFYSSIRTSNNSQVNKLTLSDESTLIEDGGARSDGSLEDGDDVH
RAVDNERDGVTSYSFFHFMLFLASLYIMMTLTNWSRYEPSREMKSQWTAVVWKISSSWIGI
VLYVWTLVAPLVLTNRDFD

FIGURE 42

GCGAGAAAGAAGCTGTCTCCATCTTGTCTGTATCCCGCTGCTTCTTGNGACGTTGTGGAGAT
GGGGAGCGTCCCTGGGGCTGTGCTCCATGGCGAGCTGGATACCATGTTTGTGTGGAAGTGCC
CCGTGTTTGCTATGCCGATGCTGTCCTAGTGGAACAANTCCACTGTAACTAGATTGATCTA
TGCACTTTTCTTGCTTGTTGGAGTATGTGTAGCTTGTGTAATGTTGATACCAGGAATGGAAG
AACAACTGAATAAGATTCCCTGGATTTTGTGAGAATGAGAAAGGTGTTGTCCCTTGTAACATT
TTGGTTGGCTATAAAGCTGTATATCGTTTGTGCTTTGGTTTGGCTATGTTCTATCTTCTTCT
CTCTTTACTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGCACAATGGAT
TTTGGTTCTTTAAATTTGCTGCAGCAATTGCAATTATTATTGGGGC

FIGURE 43

GTTATTGTGAACTTTGTGGAGATGGGAGGTCNTGGGGCTGTGTTCCATGGCGAGCTGGATAC
CANGTTTGTGTGGAAGTGCCCCGTGTTTGNTATGCCGATGCTGTCCTAGTGGAACAANTCC
ACTGTAATTAGATTGATNTATGCACTTTTNTTGCTTGTTGGAGTANGTGTAGCTTGTGTAAT
GTTGATACCAGGAATGGAAGAACAACGAATAAGATTCCTGGATTTTGTGAGAATGAGAAAG
GTGTTGTCCCTTGTAACATTTTGGTTGGCTATAAAGCTGTATATNGTTTGTGCTTTGGTTTG
GCTANGTTCTATNTTCTTCTCTCTTTACTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAG
AGCTGCAGTGCACAATGGATTTTGGTTTTTTAAATTGCTGCAGCAATTGCAATTATTATTG
GGGC

FIGURE 44

AAGAAGCTGTCTCCATCTTGTCTGTATCCGCTGCTCTTGTGAACGTTNTGGAGATGGGGAGC
GTCCTTGGGGTTGTGCTCCATGGCGAGCTGGATACCATGTTTGTGTGGAAGTGCCCCGTGTT
TGCTATGCCGATGCTGTCCTAGTGGAAACAACCTCCACTGTAAC TAGATTGATCTATGCACTT
TTCTTGCTTGTTGGAGTATGTGTAGCTTGTGTAATGTTGATACCAGGAATGGAAGAACAAC
GAATAAGATTCCCTGGATTTTGTGAGAATGAGAAAGGTGTTGTCCCTTGTAACATTTTGGTTG
GCTATAAAGCTGTATATCGTTTGTGCTTTGGTTTGGCTATGTTCTATCTTCTTCTCTTTA
CTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGCACAATGGATTTTGGTT
CTTTAAATTTGCTGCAGCAATTGCAATTATTATTGGGGC

GCTGTCCTTAGTGGAACAANTCCAACCTTGTAACCTTGGATTGATCTATGCACCTTTTTTCCCTTG
CTTGTTGGAGTATGTGTAGCTTTGTGTAAATGTTGTTCCAGGATTGGANGAACAACTGAATA
AGATTCCTGGATTTTTGTGAGAATGAGAAAGGTGTTGTCCCCTTGTAACATTTTTGGTTGGC
TATAAAGCTGTATATCGTTTGTGCTTTGGTTTGGCTATGTTCTATCTTCTTCTCTTTACT
AATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGCACAATGGATTTTTGGTTCT
TTAAATTTGCTGCAGCAATTGCAATTATTATTGGGGCATTCTTCATTCCAGAAGGAACTTTT
ACAACTGTGTGGTTTTATGTAGGCATGGCAGGTGCCTTTTGTTCATCCTCATACAACTAGT
CTTACTTATTGATTTTGCACATTCATGGAATGAATCGTGGGTGAAAAAATGGAAGAAGGGA
ACTCGAGATGTTGGTATGCAGCCTTGTTATCAGCTACAGCTCTGAATTATCTGCTGTCTTTA
GTTGCTATCGTCCTGTTCTTTGTCTACTACACTCATCCAGCCAGTTGTTTCAGAAAACAAGGC
GTTTCATCAGTGTCAACATGCTCCTCTGCGTTGGTGCTTCTGTAATG

CTCGGGCGCGCACAGGCAGCTCGGTTTGCCTGCGATTGAGCTGCGGGTGCGGCGCGCGCGGCTCTCCAAT
GGCAAATGTGTGTGGCTGGAGGCGAGCGCGAGGCTTTTCGCAAAGGCAGTCGAGTGTTTGCAGACCGGGGCGAG
TCCTGTGAAAGCAGATAAAAAGAAAACATTTATTAACGTGTCAATTACGAGGGGAGCGCCCGGGCGGGGCTGTGCG
ACTCCCCGCGGAACATTTGGCTCCCTCCAGCTCCGAGAGAGGAGAAGAAGAAAGCGGAAAAGAGGCAGATTAC
GTCGTTTCCAGCCAAGTGGACCTGATCGATGGCCCTCCTGAATTTATCACGATATTTGATTTATAGCGATGCC
CCCTGGTTTGTGTGTTACGCACACACAGTCGCACACAAGGCTCTGGCTCGTTCCCTCCCTCGTTTCCAGCTCC
TGGGCGAATCCCACATCTGTTTCACTCTCCGCCGAGGGCGAGCAGGAGCGAGAGTGTGTGCAATCTGCGAGTG
AAGAGGGACGAGGGGAAAAGAAACAAAGCCACAGACGCAACTTGAGACTCCCGCATCCCAAAGAAGCACCAGAT
CAGCAAAAAAAGAAGATGGGCCCCCCCCGAGCCTCGTGCTGTGCTTGCTGTCCGCAACTGTGTTCTCCCTGCTGGG
TGGAAGCTCGGCCCTTCTGTGCGACCACCGCCTGAAAGGCAGGTTTCAGAGGGACCGCAGGAACATCCGCCCA
ACATCATCCTGGTGCTGACGGACGACCAGGATGTGGAGCTGGGTTCATGCAAGTGATGAACAAGACCCGGCGC
ATCATGGAGCAGGGCGGGGCGCACTTCACTCAACGCCTTCGTACCACACCCATGTGCTGCCCTCAGCTCCTC
CATCCTCACTGGCAAGTACGCTCCAAACCAACACACTACCAACAATGAGAAGTGTCTCCTCGCCCTCCTGGC
AGGCACAGCAGCAGAGAGCCGACCTTTGGCGTGTACCTCAATAGCACTGGCTACCGGACAGCTTTCTTCGGGAAG
TATCTTAATGAATACAACGGCTCCTACGTGCCACCCGGCTGGAAGGAGTGGGTGCGACTCCTTAAAAACTCCCG
CTTTTATAACTACACGCTGTGTGCGAACGGGGTGAAAGAGAAGCACGGCTCCGACTACTCCAAGGATTACCTCA
CAGACCTCATACCAATGACAGCGTGAGCTTCTTCCGCACGTCCAAGAAGATGTACCCGCACAGGCCAGTCCCTC
ATGGTCATCAGCCATGCAGCCCCCCCCACGGCCCTGAGGATTCAGCCCCACAATTCACGCTCTTCCCCAACGC
ATCTCAGCACATCAGCCGAGACTACAACACGCGCCCAACCGGACAACACCTGGATCATGCGCTACACGGGGC
CCATGAAGCCCCATCCATGGAATTCACCAACATGCTCCAGCGGAAGCGCTTGACAGCCCTCATGTGCGTGGAC
GACTCCATGGAGACGATTTACAACATGCTGGTTGAGACGGGCGAGCTGGACAACACGTACATCGTATACACCGC
CGACCACGGTTACCACATCGGCCAGTTTGGCCTGGTGAAAGGGAATCCATGCCATATGAGTTTGACATCAGGG
TCCCGTTCTACGTGAGGGGGCCCCAACGTGGAAGCCGGCTGTCTGAATCCCCACATCGTCTCTCAACATTGACCTG
GCCCCACCATCCTGGACATTTGCAGGCCTGGACATACCTGCGGGATATGGACGGGAAATCCATCCTCAAGCTGT
GGACACGGAGCGGCGCGGTGAATCGGTTTCACTTGAAAAGAAGATGAGGGTCTGCGGGGACTCCTTCTTGGTGG
AGAGAGGCAAGCTGCTACACAAGAGAGACATGACAAGGTGGACGCCAGGAGGAGAAGTTTCTGCCAAGTAC
CAGCGTGTGAAGGACCTGTGTGACGCTGTGAGTACCAGACGGCGTGTGAGCAGCTGGGACAGAAGTGGCAGTG
TGTGGAGGACGCCACGGGGAAGCTGAAGCTGCATAAGTGCAAGGGCCCCATGCGGCTGGGCGGCAGCAGAGCCC
TCTCCAACCTCGTGCCCAAGTACTACGGGCAGGGCAGCGAGGCCTGCACCTGTGACAGCGGGGACTACAAGCTC
AGCCTGGCCGGACGCCGGAATACTCTTCAAGAAGAAGTACAAGGCCAGCTATGTCCGAGTGCCTCCATCCG
CTCAGTGGCCATCGAGGTGGACGGCAGGGTGTACACGTAAGCCTGGGTGATGCCGCCACGCCGAAACCTCA
CCAAGCGGCACTGGCCAGGGGCCCTGAGGACCAAGATGACAAGGATGGTGGGACTTCAGTGGCACTGGAGGC
CTTCCCAGTACTACGCGGCCAACCCCATTAAGTGCACATCGGTGCTACATCCTAGAGAACGCACAGTCCA
GTGTGACCTGGACCTGTACAAGTCCCTGCAGGCCTGGAAAGACCACAAGCTGCACATCGACCAGAGATTGAAA
CCCTGCAGAACAAAATTAAGAACCTGAGGGAAGTCCGAGGTCACTGAAGAAAAAGCGGCCAGAAGAATGTGAC
TGTACAAAATCAGCTACCACACCCAGCACAAAGGCCGCCTCAAGCACAGAGGCTCCAGTCTGCATCCTTTTCAG
GAAGGGCCTGCAAGAGAAGGACAAGGTGTGGCTGTTGCGGGAGCAGAAGCGCAAGAAGAACTCCGCAAGCTGC
TCAAGCGCCTGCAGAACACAGACAGTGCAGCATGCCAGGCCTCAGTGTCTTACCCACGACACCCAGCACTGG
CAGACGGCGCTTCTTGACACTGCGGCCCTTTCTGTGCTGCAACAGCGCCAACAATAACACGTACTGGTGCAT
GAGGACCATCAATGAGACTCACAATTTCTCTTCTGTGAATTTGCAACTGGCTTCTAGAGTACTTTGATCTCA
ACACAGACCCCTACCAGCTGATGAATGCAGTGAACACACTGGACAGGGATGTCCTCAACCAGCTACACGTACAG
CTCATGGAGCTGAGGAGCTGCAAGGTTACAAGCAGTGTAACCCCCGGACTCGAAACATGGACCTGGATGGAGG
AAGCTATGAGCAATACAGGCAGTTTCAGCGTTCGAAAGTGGCCAGAAATGAAGAGACCTTCTTCCAATCACTGG
GACAACCTGTGGGAAGCTGGGAAGGTTAAGAAACAACAGAGGTGGACCTCCAAAAACATAGAGGCATCACTGTA
CTGCACAGGCAATGAAAAACCATGTGGGTGATTTCCAGACAGCTGTGCTATTGGCCAGGAGGCTGAGAAAGC
AAGCAGCACTCTCAGTCAACATGACAGATTCTGGAGGATAACCAGCAGGAGCAGAGATAACTTCAGGAAGTCC
ATTTTTGCCCTGCTTTTGCTTTGGATTATACCTCACCAGCTGCACAAAATGCATTTTTTCGTATCAAAAAGTC
ACCACTAACCTCCCCAGAAGCTCACAAGGAAAACGGAGAGAGCGAGCGAGAGAGATTTCTTGGAAATTC
TCCAAGGGCGAAAGTCATTGGAATTTTTAAATCATAGGGGAAAAAGCAGTCTGTTCTAAATCCTCTTATCTT
TTGGTTTGTACAAAAGAAGAACTAAGAAGCAGGACAGGCAACGTGGAGAGGCTGAAAACAGCTGCAGAGACG
TTTGACAATGAGTCAGTAGCACAAGAGATGACATTTTACCTAGCACTATAAACCTGGTTGCTCTGAAGAAA
CTGCCTTCATGTATATATGTGACTATTTACATGTAATCAACATGGAACTTTTAGGGGAACCTAATAAGAAAT
CCCAATTTTCAGGAGTGGTGGTGTCAATAAACGCTCTGTGGCCAGTGTAAAAGAAAAA

FIGURE 47

MGPPSLVLCLLSATVFSLLGGSSAFLSHHRLKGRFQRDRRNIRPNIILVLTDDQDVELGSMQ
VMNKTRRIMEQGGAHFINAFVTTMCCPSRSSILTGKYVHNHNTYTNNECSPSWQAQHE
RTFAVYLNSTGYRTAFFGKYLNEYNGSYVPPGWKEWVGLLKNSRFYNYTLCRNGVKEKHGSD
YSKDYLTDLITNDSVSFFRTSKKMPHRPVLVISHAAPHGPEDSAPQYSRLFPNASQHITP
SYNYAPNPDKHWMRYTGPMKPIHMEFTNMLQRKRLQTLMSVDDSMETIYNMLVETGELDNT
YIVYTADHGYHIGQFGLVKGKSMPYEFDIRVPFYVRGPNVEAGCLNPHIVLNIDLAPTILDI
AGLDIPADMDGKSILKLLDTERPVNRFHLKKKMRVWRDSFLVERGKLLHKRDNDKVDAQEEN
FLPKYQRVKDLQCRAEYQTACEQLGQKWQCVEDATGKCLKHKCKGPMRLGGSRALSNLVPKY
YGQGSEACTCDSDYKLSLAGRRKKLFKKKYKASYVRSRSIRSVAI EVDGRVYHVGLGDAAQ
PRNLTKRHWP GAPPEDQDDKDGGDFSGTGGLPDYSAANPIKVTHRCYILENDTVQCDLDLYKS
LQAWKDHKLHIDHEIETLQNKIKNLREVRGHLKKKRPEECDCHKISYHTQHKGRCLKHRGSSL
HPFRKGLQEKDKVWLLREQKRKKLRKLLKRLQNNDTCSMPGLTCFTHDNQHWQTAPFWTLG
PFCACTSANNNTYWCMRTINETHNLFCEFATGFLEYFDLNTDPYQLMNAVNTLDRDVLNQL
HVQLMELRSCKGYKQCNPRTRNMDLDGGSYEQYRQFQRRKWPEMKRPSSKSLGQLWEGWEG

FIGURE 48

AACAAAGTTCAGTGACTGAGAGGGCTGAGCGGAGGCTGCTGAAGGGGAGAAAGGAGTGAGGA
GCTGCTGGGCAGAGAGGGGACTGTCCGGCTCCCAGATGCTGGGCCTCCTGGGGAGCACAGCCC
TCGTGGGATGGATCACAGGTGCTGCTGTGGCGGTCCTGCTGCTGCTGCTGCTGCTGGCCACC
TGCCTTTTCCACGGACGGCAGGACTGTGACGTGGAGAGGAACCGTACAGCTGCAGGGGGAAA
CCGAGTCCGCCGGGGCCCAGCCTTGGCCCTTCCGGCGGGGGGCCACCTGGGAATCTTTCACC
ATCACCGTCATCCTGGCCACGTATCTCATGTGCCGAATGTGGGCCTCCACCACCACCACCAC
CCCCGCCACACCCCTCACCACCTCCACCACCACCACCACCCCCACCGCCACCATCCCCGCCA
CGCTCGCTGAGGCTGCTGTGCGCCGGTGCCTGTGGACAGCAGCTGCCCCCTGCCCTCCCATCTG
TTCCCAGGACAAGTGGACCCCATGTTTCCATGTGGAAGGATGCATCTCTGGGGTGAACGAGG
GGAACAATAGACTGGGGCTTGCTCCAGCTGCATTTGCATGGCATGCCCCAGTGTACTATGGC
AGCAGAGAATGGAGGAACACTGGGTCTGCAGTGCTGAAGGGTTTGGGGAGTGGAGAGCAAGG
GTGCTCTTTCGGGGCTGGACAGCCCGTCTTGTGACAGTGACTCCCAGTGAGCCCCAGAAATG
ACAAGCGTGTCTTGGCAGAGCCAGCACACAAGTGGATGTGAAGTGCCCGTCTTGACCTCCTC
ATCAGGCTGCTGCAGGCCTCTGGCGGGCAGGGCACTGGGAGAGGCCCTGAGAATGTCCTTTT
GGTTTGGAGAAGGCAGTGTGAGGCTGCACAGTCAATTCATCGGTGCCTTAGTCCAAGAAAAT
AAAAACCACTAAGAAGCTTTAAAAAAAAAAAAAAAAAAAAA

MLGLLGSTALVGWITGA AVAVLLLLLLLLLATCLFHGRQDCDVERNRTAAGGNRVRR AQPWPFR
RRGHLGIFHHHRHPGHVSHVPNVGLHHHHHPRHTPHHLHHHHHPHRHHPRHAR

FIGURE 50

GGCGGCTGCTGAGCTGCCTTGAGGTGCAGTGTTGGGGATCCAGAGCC**ATG**TCGGACCTGCTA
CTACTGGGCCTGATTGGGGGCCTGACTCTCTTACTGCTGCTGACGCTGCTGGCCTTTGCCGG
GTACTCAGGGCTACTGGCTGGGGTGAAGTGAGTGCTGGGTACCCCCCATCCGCAACGTCA
CTGTGGCCTACAAGTTCCACATGGGGCTCTATGGTGAGACTGGGCGGCTTTTCACTGAGAGC
TGCAGCATCTCTCCCAAGCTCCGCTCCATCGCTGTCTACTATGACAACCCCCACATGGTGCC
CCCTGATAAGTGCCGATGTGCCGTGGGCAGCATCCTGAGTGAAGGTGAGGAATCGCCCTCCC
CTGAGCTCATCGACCTCTACCAGAAATTTGGCTTCAAGGTGTTCTCCTTCCCGGCACCCAGC
CATGTGGTGACAGCCACCTTCCCCTACACCACCATTTCTGTCCATCTGGCTGGCTACCCGCCG
TGTCCATCCTGCCTTGGACACCTACATCAAGGAGCGGAAGCTGTGTGCCTATCCTCGGCTGG
AGATCTACCAGGAAGACCAGATCCATTTTCATGTGCCCACTGGCACGGCAGGGAGACTTCTAT
GTGCCTGAGATGAAGGAGACAGAGTGGAAATGGCGGGGGCTTGTGGAGGCCATTGACACCCA
GGTGGATGGCACAGGAGCTGACACAATGAGTGACACGAGTTCTGTAAGCTTGGAAGTGAGCC
CTGGCAGCCGGGAGACTTCAGCTGCCACACTGTCACCTGGGGCGAGCAGCCGTGGCTGGGAT
GACGGTGACACCCGCAGCGAGCACAGCTACAGCGAGTCAGGTGCCAGCGGCTCCTCTTTTGA
GGAGCTGGACTTGAGGGGCGAGGGGCCCTTAGGGGAGTCACGGCTGGACCCTGGGACTGAGC
CCCTGGGGACTACCAAGTGGCTCTGGGAGCCCACTGCCCCTGAGAAGGGCAAGGAG**TAA**CCC
ATGGCCTGCACCCTCCTGCAGTGCAGTTGCTGAGGAAGTGAAGGAGTCTCCAGCAGACTCT
CCAGCCCTCTTCCTCCTCCTCTGGGGGAGGAGGGGTTTCTGAGGGACCTGACTTCCCCTGC
TCCAGGCCTCTTGCTAAGCCTTCTCCTCACTGCCCTTTAGGCTCCCAGGGCCAGAGGAGCCA
GGGACTATTTTCTGCACCAGCCCCCAGGGCTGCCGCCCTGTTGTGTCTTTTTTTCAGACTC
ACAGTGAGCTTCCAGGACCCAGAATAAAGCCAATGATTTACTTGTTTCACCTGGAAAAAA
AAAAAAA

FIGURE 51

MSDLLLLGLIGGLTLLLLLTLLAFAGYSGLLAGVEVSAGSPPIRNVTVAYKFHMGLYGETGR
LFTESCSISPKLRSIAYYYDNPHMVPPDKCRAVGSI LSEGEESPSPELIDLYQKFGFKVFS
FPAPSHVVTATFPYTTILSIWLATR RVHPALDTYIKERKLCAYPRLEIYQEDQIHFMCP LAR
QGDFYVPEMKETEWKWRGLVEAIDTQVDGTGADTMSDTSSVSLEVSPGSRETS AATLSPGAS
SRGWDDGDTRSEHSYSESGASGSSFEELDLEGEGLGESRLDPGTEPLGTTKWLWEPTAPEK
GKE

099434-44464
T0944-44464

FIGURE 52

CCGCGGGAACGCTGTCTGGCTGCCGCCACCCGAACAGCCTGTCTGGTGCCCCGGCTCCCT
GCCCCGCGCCAGTC**ATG**ACCCTGCGCCCCTCACTCCTCCCGCTCCATCTGCTGCTGCTGCT
GCTGCTCAGTGCGGCGGTGTGCCGGGCTGAGGCTGGGCTCGAAACCGAAAGTCCCGTCCGGA
CCCTCCAAGTGAGAGCCCTGGTGGAGCCCCCAGAACCATGTGCCGAGCCCGCTGCTTTTGGA
GACACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACGTATTATTGACACCTCCCT
GACCAGAGACCCTCTGGTTATAGAACTTGGCCAAAAGCAGGTGATTCCAGGTCTGGAGCAGA
GTCTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATTCTTCTCACTTGGCCTAT
GGAAAACGGGGATTTCCACCATCTGTCCCAGCGGATGCAGTGGTGCAGTATGACGTGGAGCT
GATTGCACTAATCCGAGCCAACTACTGGCTAAAGCTGGTGAAGGGCATTTTGCTCTGGTAG
GGATGGCCATGGTGCCAGCCCTCCTGGGCCTCATTTGGGTATCACCTATACAGAAAGGCCAAT
AGACCCAAAGTCTCCAAAAGAAGCTCAAGGAAGAGAAACGAAACAAGAGCAAAAAGAA**TA**
ATAAATAATAAATTTTAAAAAACTTAAAAAAAAAAAAAAAAAAAA

FIGURE 53

MTLRPSLLPLHLLLLLLLLSAAVCRAEAGLETESPVRTLQVETLVEPPEPCAEPAAFCDTLHI
HYTGSLVDGRIIDTSLTRDPLVIELGQKQVIPGLEQSLLDMCVGEKRRAIIPSHLAYGKRGF
PPSVPADAVVQYDVELIALIRANYWLKLVKGILPLVGMAMVPALLGLIGYHLYRKANRPKVS
KKKLKEEKRNKSKKK

TCGTTT TGTGSD

FIGURE 54

CCCGGGAACGTGTTTCCTGGCTGCCGCACCCGAACAGCCTGTCCTGGTGCCCCGGCTCCCTGC
CCCGCGCCCAGTCATGACCCTGCGCCCCCTCACTCCTCCCGCTCCATCTGCTGCTGCTGCTGC
TGCTCAGTGCGGCGGTGTGCCGGGCTGAGGCTGGGCTCGAAACCGAAAGTCCCGTCCGGACC
CTCCAAGTGGAGACCCTGGTGGAGCCCCCAGAACCATGTGCCGAGCCCGCTGCTTTTGGAGA
CACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACGTATTATTGACACCTCCCTGA
CCAGAGACCCTCTGGTTATAGAACTTGGCCAAAAGCAGGTGATTCCAGGTCTGGAGCAGAGT
CTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATTCCTTCTCACTTGGCCTATGG
AAAACGGGGATTTCCACCATCTGTCCCAGCGGATGCAGTGGTGCAGTATGACGTGGAGCTGA
TTGCACTAATCCGAGCCAACTACTGGCTAAAGCTGGTGAAGGGCATTTTGCCTCTGGTAGGG
ATGGCCATGGTGCCACCCTCCTGGGCCTCATTGGGTATCACCTATACAGAAAGGCCAATAGA
CCCAAAGTCTCCAAAAGAAGCTCAAGGAAGAGAAACGAAACAAGAGCAAAAAGAAATAATA
AATAATAAATTTTAAAAAACTTA

FIGURE 55

CCGAAAGTCCCGTCCGGACCCCTCCAAGTGGAGACCCCTGGTGGAGCCCCCAGAACCATGTGCC
GAGCCCGCTGCTTTTGGAGACACGCTTCACATACTACACGGGAAGCTTGGTAGATGGACG
TATTATTGACACCTCCCTGACCAGAGACCCCTCTGGTTATAGAACTTGGCCAAAAGCAGGTGA
TTCCAGGTCTGGAGCAGAGTCTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATT
CCTTCTCACTTGGCCTATGGAAAACGGGGATTTCCACCATCTGTCCCAGCGGATGCAGTGGT
GCAGTATGACGTGGAGCTGATTGCACTAATCCGAGCCAACTACTGGCTAAAGCTGGTGAAGG
GCATTTTGCCTCTGGTAGGGATGGCCATGGTGCCAGCCCTCCTGGGCCTCATTGGGTATCAC
CTATACAGAAAGGCCAATAGACCCAAAGTCTCCAAAAGAAGCTCAAGGAAGAGAAACGAAA
CAAGAGCAAAAAGAAATAATAATAATAAATTTAAAAAACTTAAAA

FIGURE 56

CTGCTGCATCCGGGTGTCTGGAGGCTGTGGCCGTTTTGTTTTCTTGGCTAAAATCGGGGGAG
TGAGGCGGGCCGGCGCGGCGGACACCGGGCTCCGGAACCACTGCACGACGGGGCTGGACTG
ACCTGAAAAAAATGTCTGGATTTCTAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGG
GAAAAGCGCAATACTATTGCTTCCATTGCTGCTGGTGTACTATTTTTTACAGGCTGGTGGAT
TATCATAGATGCAGCTGTTATTTATCCACCATGAAAGATTTCAACCACTCATACCATGCCT
GTGGTGTATAGCAACCATAGCCTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGA
GGTGATAGTTACAGTGAAGGTTGTCTGGGTCAAACAGGTGCTCGCATTTGGCTTTTCGTTGG
TTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGGATTCTTTTTGGAGGTTATGTTG
CTAAAGAAAAAGACATAGTATACCCTGGAATTGCTGTATTTTTCCAGAATGCCTTCATCTTT
TTTGGAGGGCTGGTTTTTAAGTTTGGCCGCACTGAAGACTTATGGCAGTGAACACATCTGAT
TTCCACAGCACAACAGCCCTGCATGGGTTTGTGTTTTTTTTACTGCTCACTCCCAACCTT
TTGTAATGCCATTTTCTAAACTTATTTCTGAGTGTAGTCTCAGCTTAAAGTTGTGTAATACT
AAAATCACGAGAACACCTAAACAACAACCAAAAATCTATTGTGGTATGCACCTGATTAACTT
ATAAAATGTTAGAGGAACTTTCACATGAATAATTTTTGTCAAATTTTATCATGGTATAATT
TGTA AAAAATAAAAAGAAATTACAAAAGAAATTATGGATTTGTCAATGTAAGTATTTGTCATA
TCTGAGGTCCAAAACCACAATGAAAGTGCTCTGAAGATTTAATGTGTTTATTCAAATGTGGT
CTCTTCTGTGTCAAATGTTAAATGAAATATAAACATTTTTTTAGTTTTTTAAATATTCCGTGG
TCAAAATTCTTCCTCACTATAATTGGTATTTACTTTTACC AAAAATTCTGTGAACATGTAAT
GTAAC TGGCTTTTGGAGGTCTCCCAAGGGGTGAGTGGACGTGTTGGAAGAGAGAAGCACCAT
GGTCCAGCCACCAGGCTCCCTGTGTCCCTTCCATGGGAAGGTCTTCCGCTGTGCCTCTCATT
CCAAGGGCAGGAAGATGTGACTCAGCCATGACACGTGGTTCTGGTGGGATGCACAGTCACTC
CACATCCACCACTG

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FIGURE 57

MSGFLEGLRCSECIDWGEKRNTIASIAAGVLFFTGWIIIDA AVIYPTMKDFNHSYHACGVI
ATIAFLMINAVSNGQVRGDSYSEGCLGQTGARIWLFVGFMLAFGSLIASMWILFGGYVAKEK
DIVYPGIAVFFQNAFIFFGGLVFKFGRTEDLWQ

SECRET

FIGURE 58

TTCTTGGCTAAAATCGGGGGAGTGAGGCGGGCCGGCGCGGCGGACACCGGGCTCCGGAACC
ACTGCACGACGGGGCTGGACTGACCTGAAAAAATGTCTGGATTTCTAGAGGGCTTGAGATG
CTCAGAATGCATTGACTGGGGGGAAAAGCGCAATACTATTGCTTCCATTGCTGCTGGTGTAC
TATTTTTTTACAGGCTGGTGGATTATCATAGATGCAGCTGTTATTTATCCCACCATGAAAGAT
TTCAACCACTCATACCATGCCTGTGGTGTATAGCAACCATAGCCTTCCTAATGATTAATGC
AGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTTGTCTGGGTCAAACAGGTG
CTCGCATTTGGCTTTTCGTTGGTTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGG
ATTCTTTTTGGAGGTTATGTTGCTAAAGAAAAAGACATAGTATACCCTGGAATTGCTGTATT
TTTCCAGAATGCCTTCATCTTTTTTTGGAGGGCTGGTTTTTTAAGTTTGGC

FIGURE 59

TGGACGGACCTGAAAAAATGTTTGGATTTNTAGAGGGNTTGAGATGTTTCAGAATGCATGAC
TGGGGGAAAAGCGCAAATACTATTGCTTCCATTGCTGCTGGTGTANTATTTTTTACAGGCTG
GTGGATTATCATAGATGCAGNTGTTATTTATCCCACCATGAAAGATTTCAACCANTCATACC
ATGCCTGTGGTGTTATAGCAACCATAGCCTTCNTAATGATTAATGCAGTATCGAATGGACAA
GTCCGAGGTGATAGTTACAGTGAAGGTTGTTTGGGTCAAACAGGTGCTCGCATTTGGCTTTT
CGTTGGTTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGGATTCTTTTTGGAGGTT
ATGTTGCTAAAGAAAAAGACATAGTATACCCTGGAATTGNTGTATTTTTCCAGAATGCCTTC
ATCTTTTTTGGAGGGCTGGTTTTTAAGTTTGGCCGCACTGAAGANTTATGGCAGTG

TGGATTTTGGAGGGCTGGTTTTTAAGTTTGGCCGCACTGAAGANTTATGGCAGTG

GGACACCGGGTTCCGGACCAATGCANGACGGGGTGGANTGACCTGAAAAAATGTTTGGATT
TTTAGAGGGCTTGAGATGNTCAGAATGCATTGACTGGGGGAAAAGCGCAATANTATTGCTTT
CCATTGCTGCTGGTGTACTATTTTTTACAGGGTGGTGGATTATCATAGATGCAGCTGTTATT
TATCCCACCATGAAAGATTTNAACCACTCATACCATGCCTGTGGTGTATAGCAACCATAGC
CTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTT
GTTTGGGTCAAACAGGTGNTCGCATTTGGCTTTTCGTTGGTTTCATGTTGGCCTTTGGATTT
CTGATTGNATTCTATGCGGATTCTTCTTGGAGGTTATGTTGCTAAAGAAAAGACATAGTAT
ACCCTGGAATTNCTNTATTTTTCCAGAATGCC

FIGURE 61

TAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGGGAAAAGCGCAATANTATTGCTTCC
ATTGNTGNTGGTGTANTATTTTTTTACAGGCTGGTGGATTATNATAGATGCAGCTGTTATTT
ATCCCACCATGAAAGATTTNAACCANTCATACCATGCCTGTGGTGTATAGCAACCATAGCC
TTCCTAATGATTAATGCAGTATNGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTTG
TTTGGGTCAAACAGGTGNTNGCATTTGGCTTTTNGTTGGTTTCATGTTGGCCTTTGGATCTN
TGATTGCATTTATGTGGATTNTTTTTGGAGGTTATGTTGCTAAAGNAAAAGACATAGTATAC
CCTGT

FIGURE 62

GGGAGGCTGTGNCCGTTTTGTTTTNTTGGCTAAAATCGGGGGAGTGAGGCGGCCCGGCGCGG
CGNGACACCGGGTTCCGGGAACCATTCACGACGGGGTGGACTGACCTGAAAAAATGTTTG
GATTTNTAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGGGAAAAGCGCAATACTATT
GCTTCCATTGCTGCTGGTGTACTATTTTTTACAGGCTGGTGGATTATCATAGATGCAGCTGT
TATTTATCCCACCATGAAAGATTTCAACCACTCATACCATGCCTGTGGTGTTATAGCAACCA
TAGCCTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAA
GGTTGTCTGGGTCAAACAGGTGCTCGCATTTGGCTTTTCGTTGGTTTCATGTTGGCCTTTGG
ATNTCTGATTGCATCTATGTGGATTCTTTTTGGAGGTTATGTTGCTAAAGAAAAAGACATAG
TATACCCTGGAATTGCTGTATTTTTCCAGAATGCCTTCATNTTTTTTGGAGGGCTG

FIGURE 63

CGACGCCGGCGT**GATG**TGGCTTCCGCTGGTGTCTGCTCCTGGCTGTGCTGCTGCTGGCCGTCC
TCTGCAAAGTTTACTTGGGACTATTCTCTGGCAGCTCCCCGAATCCTTTCTCCGAAGATGTC
AAACGGCCCCCAGCGCCCCCTGGTAAGTACAAAGGAGGCCAGGAAGAAGGTTCTCAAACAAGC
TTTTTTCAGCCAACCAAGTGCCGGAGAAAGCTGGATGTGGTGGTAATTGGCAGTGGCTTTGGGG
GCCTGGCTGCAGCTGCAATTCTAGCTAAAGCTGGCAAGCGAGTCCTGGTGTGGAACAACAT
ACCAAGGCAGGGGGCTGCTGTCATACCTTTGGAAAGAATGGCCTTGAATTTGACACAGGAAT
CCATTACATTTGGGCGTATGGAAGAGGGCAGCATTGGCCGTTTTATCTTGGACCAGATCACTG
AAGGGCAGCTGGACTGGGCTCCCCTGTCCTCTCTCTTTTGGACATCATGGTACTGGAAGGGCCC
AATGGCCGAAAGGAGTACCCCATGTACAGTGGAGAGAAAGCCTACATTACAGGGCCTCAAGGA
GAAGTTTCCACAGGAGGAAGCTATCATTGACAAGTATATAAAGCTGGTTAAGGTGGTATCCA
GTGGAGCCCCCTCATGCCATCCTGTTGAAATTCCTCCCATTGCCCCGTGGTTTCAGCTCCTCGAC
AGGTGTGGGCTGCTGACTCGTTTCTCTCCATTCTTCAAGCATCCACCCAGAGCCTGGCTGA
GGTCTGCGAGCAGCTGGGGGCCCTCCTCTGAGCTCCAGGCAGTACTCAGCTACATCTTCCCCA
CTTACGGTGTACCCCCAACCACAGTGCCTTTTCCATGCACGCCCTGCTGGTCAACCACTAC
ATGAAAGGAGGCTTTTATCCCCGAGGGGGTTCCAGTGAAATTGCCTTCCACACCATCCCTGT
GATTCAGCGGGCTGGGGGGCTGTCCTCACAAAGGCCACTGTGCAGAGTGTGTTGCTGGACT
CAGCTGGGAAAGCCTGTGGTGTGAGTGTGAAGAAGGGGCATGAGCTGGTGAACATCTATTGC
CCCATCGTGGTCTCCAACGCAGGACTGTTCAACACCTATGAACACCTACTGCCGGGAACGC
CCGCTGCCCTGCCAGGTGTGAAGCAGCAACTGGGGACGGTGC GGCCCCGGCTTAGGCATGACCT
CTGTTTTTCTGCTGCGTGCAGGACCAAGGAAGACCTGCATCTGCCGTCCACCAACTACTAT
GTTTACTATGACACGGACATGGACCAGGCGATGGAGCGCTACGTCTCCATGCCAGGGAAGA
GGCTGCGGAACACATCCCTCTTCTTCTTCTCGCTTTCCCATCAGCCAAAGATCCGACCTGGG
AGGACCGATTCCCAGGGCCGCTCCACCATGATCATGCTCATACCCACTGCCTACGAGTGGTTT
GAGGAGTGGCAGGCGGAGCTGAAGGGAAAGCGGGGCAGTGAATATGAGACCTTCAAAAACCTC
CTTTGTGGAAGCCTCTATGTGAGTGGTCTGAAACTGTTCCACAGCTGGAGGGGAAGGTGG
AGAGTGTGACTGCAGGATCCCCACTCACCAACCAGTTCTATCTGGCTGCTCCCCGAGGTGCC
TGCTACGGGGCTGACCATGACCTGGGGCGCTGCACCCCTTGTGTGATGGCCCTCTTGAGGGC
CCAGAGCCCCATCCCCAACCTCTATCTGACAGGAGGATATCTTACCTGTGGACTGGTCG
GGGCCCTGCAAGGTGCCCTGCTGTGACAGCGCCATCCTGAAGCGGAACCTTGTACTCAGAC
CTTAAGAATCTTGATTCTAGGATCCGGGCACAGAAGAAAAAGAAT**TAGT**TCCATCAGGGAGG
AGTCAGAGGAATTTGCCCAATGGCTGGGGCATCTCCCTTGACTTACCCATAATGTCTTTCTG
CATTAGTTCCTTGACAGTATAAAGCACTCTAATTTGGTTCTGATGCCTGAAGAGAGGCCTAG
TTTAAATCACAAATCCGAATCTGGGGCAATGGAATCACTGCTTCCAGCTGGGGCAGGTGAGA
TCTTTACGCCTTTTATAACATGCCATCCCTACTAATAGGATATTGACTTGGATAGCTTGATG
TCTCATGACGAGCGGCGCTGTCATCCCTCACCCATGCCTCCTAACTCAGTGATCAAAGCGA
ATATTCCATCTGTGGATAGAACCCTGGCAGTGTGTGCTGAGCTCAACCTGGTGGGTTCAGTTC
TGTCTGAGGCTTCTGCTCTCATTCAATTTAGTGTACGCTGCACAGTTCTACACTGTCAAGG
GAAAAGGGAGACTAATGAGGCTTAACCTCAAAACCTGGGCGTGGTTTTGGTTGCCATTCCATA
GGTTTGGAGAGCTCTAGATCTCTTTTGTGCTGGGTTTCAGTGGCTCTTCAGGGGACAGGAAAT
GCCTGTGTCTGGCCAGTGTGGTTCTGGAGCTTTGGGGTAACAGCAGGATCCATCAGTTAGTA
GGGTGCATGTGAGATGATCATATCCAATTCAATGGAAGTCCCGGGTCTGTCTTCTTATCA
TCGGGGTGGCAGCTGGTTCTCAATGTGCCAGCAGGGACTCAGTACCTGAGCCTCAATCAAGC
CTTATCCACCAAATACACAGGGAAGGGTGATGCAGGGAAGGGTGACATCAGGAGTCAGGGCA
TGGACTGGTAAGATGAATACTTTGCTGGGCTGAAGCAGGCTGCAGGGCATTCCAGCCAAGGG
CACAGCAGGGGACAGTGCAGGGAGGTGTGGGGTAAGGGAGGGAAGTCACATCAGAAAAGGGA
AAGCCACGGAATGTGTGTGAAGCCCAGAAATGGCATTTCAGTGAATTAGCACATGTGAGGG
TTAGACAGGTAGGTGAATGCAAGCTCAAGGTTTGGAAAAATGACTTTTCAGTTATGTCTTTG
GTATCAGACATACGAAAGGTCTCTTTGTAGTTCGTGTTAATGTAAACATTAATAAATTTATTG
ATTCCATTGCTTTAAAAA

MWLPVLVLLLAVLLLAVLCKVYVLGLFSGSSPNPFSEVDKRPAPLVTDKARKKVLKQAFSAN
QVPEKLDVVVIGSGFGGLAAAAILAKAGKRVLVLEQHTKAGGCCHTFGKNGLEFDTGIHYIG
RMEEGSIGRFILDQITEGQLDWAPLSSPFDIMVLEGPNGRKEYPMYSGEKAYIQGLKEKFPQ
EEAII DKYIKLVKVVS SGAPHAILLKFLPLPVVQLLDRCGLLTRFSPFLQASTQSLAEVLQQ
LGASSELQAVLSYIFPTYGVTPNHSAFSMHALLVNHYMKGGFYPRGGSSEIAFHTIPVIQRA
GGAVLT KATVQSVLLDSAGKACGVSVKKGHVNIYCPIVVSNAGLFNTYEHLLPGNARCLP
GVKQQLGTVRPGLGMTSVFICLRGTKE DLHLPSTNYVYYD TMDQAMERYVSMPREEAAEH
IPLLFFAFPSAKDPTWEDRFPGRSTMIMLIPTAYEWFEWQAE LKGRGSDYETFKNSFVEA
SMSVVLKLFPPQLEGKVESVTAGSPLTNQFYLAAPRGACYGADHDLGRLHPCVMASLRAQSPI
PNLYLTGQDIFTCGLV GALQGALLCSSAILKRNLYS DLKNLDSRIRAQKKKN

[illegible]

FIGURE 66

MRVRIGLTLLLCVLLSLASASSDEEGSQDESLSKTTLTSDSVKDHTTAGRVVAGQIFLD
SEESELESSIQEEEDSLKSQEGESVTEDISFLESPNPENKDYEEPKKVRKPALTAIEGTAHG
EPCHFPFLLDKEYDECTSDGREDGRLWCATTYDYKADEKWGFCETEEEEAAKRRQMQEAEEM
YQTGMKILNGSNKKSQKREAYRYLQKAASMNHTKALERSYALLFGDYLPQNIQAAREMFEK
LTEEGSPKGQTALGFLYASGLGVNSSQAKALVYYTFGALGGNLIAHMLVLSRL

FIGURE 67

CTTCCCAGCCCTGTGCCCCAAAGCACCTGGAGCATATAGCCTTGCAGAACTTCTACTTGCCT
GCCTCCCTGCCTCTGGCC**ATG**GCCTGCCGGTGCCTCAGCTTCCTTCTGATGGGGACCTTCCT
GTCAGTTTCCCAGACAGTCCTGGCCCAGCTGGATGCACTGCTGGTCTTCCCAGGCCAAGTGG
CTCAACTCTCCTGCACGCTCAGCCCCAGCACGTCACCATCAGGGACTACGGTGTGTCTCTGG
TACCAGCAGCGGGCAGGCAGTGCCCCCTCGATATCTCCTCTACTACCGCTCGGAGGAGGATCA
CCACCGGCCTGCTGACATCCCCGATCGATTCTCGGCAGCCAAGGATGAGGCCCACAATGCCT
GTGTCCTCACCATTAGTCCCGTGCAGCCTGAAGACGACGCGGATTACTACTGCTCTGTTGGC
TACGGCTTTAGTCCC**TAG**GGGTGGGGTGTGAGATGGGTGCCTCCCCTCTGCCTCCCATTCT
GCCCCTGACCTTGGGTCCCTTTTAAACTTTCTCTGAGCCTTGCTTCCCCTCTGTAAAATGGG
TTAATAATATTCAACATGTCAACAAC

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FIGURE 68

MACRCLSFLLMGTFLSVSQTVLAQLDALLVFPQVAQLSCTLSPQHVTIRDYGVSWYQQRAG
SAPRYLLYRSEEDHHRPADI PDRFSAKDEAHNACVLTISPVPEDDADYYCSVGYGFS

FIGURE 68

FIGURE 69

GCCGCCCCGCCCCGAGACCGGGCCCCGGGGGCGCGGGGCGGCGGGATGCGGGCGCCCGGGGCGG
 CGATGACCGCGGAGCGCACGCCGCGGGCCCCGGCCCTGACCCCGCCGCCCCGCGCTGAGCCC
 CCCGCGGAGGTCCGGACAGGCCGAG**ATG**ACGCCGAGCCCCCTGTTGCTGCTCCTGCTGCCGC
 CGCTGCTGCTGGGGGCCCTTCCCCACCGGCCGCCGCCGCCGAGGCCCCCAAGATGGCGGAC
 AAGGTGGTCCACCGGCAGGTGGCCCCGGCTGGGCGGCACTGTGCGGCTGCAGTGCCAGTGGA
 GGGGGACCCGCGCCGCTGACCATGTGGACCAAGGATGGCCGCACCATCCACAGCGGCTGGA
 GCCGCTTCCGCGTGCTGCCGCAGGGGCTGAAGGTGAAGCAGGTGGAGCGGGAGGATGCCGGC
 GTGTACGTGTGCAAGGCCACCAACGGCTTCGGCAGCCTGAGCGTCAACTACACCCTCGTCGT
 GCTGGATGACATTAGCCCAGGGAAGGAGAGCCTGGGGCCCGACAGCTCCTCTGGGGGTCAAG
 AGGACCCCGCCAGCCAGCAGTGGGCACGACCGCGCTTCACACAGCCCTCCAAGATGAGGCGC
 CGGGTGATCGCACGGCCCGTGGGTAGCTCCGTGCGGCTCAAGTGCGTGCCAGCGGGCACCC
 TCGGCCCCGACATCACGTGGATGAAGGACGACCAGGCCTTGACGCGCCAGAGGCCGCTGAGC
 CCAGGAAGAAGAAGTGGACACTGAGCCTGAAGAACCTGCGGCCGGAGGACACAGCGCAAATAC
 ACCTGCCGCGTGTGCAACCGCGCGGGCGCCATCAACGCCACCTACAAGGTGGATGTGATCCA
 GCGGACCCGTTCCAAGCCCGTGTCTCACAGGCACGCACCCCGTGAACACGACGGTGGACTTCG
 GGGGGACACGTCCTTCCAGTGCAAGGTGCGCAGCGACGTGAAGCCGGTGATCCAGTGGCTG
 AAGCGCGTGGAGTACGGCGCCGAGGGCCGCCACAACCTCCACCATCGATGTGGGCGGCCAGAA
 GTTTGTGGTGCTGCCACGGGTGACGTGGTTCGCGGCCGACGGCTCCTACCTCAATAAGC
 TGCTCATCACCCGTGCCCGCCAGGACGATGCGGGCATGTACATCTGCCTTGGCGCCAACACC
 ATGGGCTACAGCTTCCGCAGCGCCTTCCTCACCGTGCTGCCAGACCCAAAACCGCCAGGGCC
 ACCTGTGGCCTCCTCGTCCTCGGCCACTAGCCTGCCGTGGCCCGTGGTTCATCGGCATCCAG
 CCGGCGCTGTCTTCATCCTGGGCACCTGCTCCTGTGGCTTTGCCAGGCCCAGAAGAAGCCG
 TGCACCCCGCGCCTGCCCTCCCCTGCTGGGCACCGCCCGCCGGGACGGCCCGCGACCCG
 CAGCGGAGACAAGGACCTTCCCTCGTTGGCCGCCCTCAGCGCTGGCCCTGGTGTGGGGCTGT
 GTGAGGAGCATGGGTCTCCGGCAGCCCCCAGCACTTACTGGGCCCAGGCCAGTTGCTGGC
 CCTAAGTTGTACCCCAAACCTCTACACAGACATCCACACACACACACACACACTCTCACAC
 AACTTCACACGTGGAGGGCAAGGTCCACCAGCACATCCACTATCAGTGCT**TAG**ACGGCACCGT
 ATCTGCAGTGGGCACGGGGGGGGCCGGCCAGACAGGCAGACTGGGAGGATGGAGGACGGAGCT
 GCAGACGAAGGCAGGGGACCCATGGCGAGGAGGAATGGCCAGCACCCAGGCAGTCTGTGTG
 TGAGGCATAGCCCCTGGACACACACACACAGACACACACACTACCTGGATGCATGTATGCAC
 ACACATGCGCGCACACGTGCTCCCTGAAGGCACACGTACGCACACGCACATGCACAGATATG
 CCGCCTGGGCACACAGATAAGCTGCCCAAATGCACGCACACGCACAGAGACATGCCAGAACA
 TACAAGGACATGCTGCCTGAACATACACACGCACACCCATGCGCAGATGTGCTGCCTGGACA
 CACACACACACACGGATATGCTGTCTGGACGCACACACGTGCAGATATGGTATCCGGACACA
 CACGTGCACAGATATGCTGCCTGGACACACAGATAATGCTGCCTTGACACACACATGCACGG
 ATATTGCCTGGACACACACACACACACACGCGTGACAGATATGCTGTCTGGACACGCACAC
 ACATGCAGATATGCTGCCTGGACACACACTTCCAGACACACGTGCACAGGCGCAGATATGCT
 GCCTGGACACACGCAGATATGCTGTCTAGTCACACACACACGCAGACATGCTGTCCGGACAC
 ACACACGCATGCACAGATATGCTGTCCGGACACACACACGCACGCAGATATGCTGCCTGGAC
 ACACACACAGATAATGCTGCCTCAACACTCACACACGTGCAGATATTGCCTGGACACACACA
 TGTGCACAGATATGCTGTCTGGACATGCACACACGTGCAGATATGCTGTCCGGATACACACG
 CACGCACACATGCAGATATGCTGCCTGGGCACACACTTCCGGACACACATGCACACACAGGT
 GCAGATATGCTGCCTGGACACACACACAGATAATGCTGCCTCAACACTCACACACGTGCAGA
 TATTGCCTGGACACACACATGTGCACAGATATGCTGTCTGGACATGCACACACGTGCAGATA
 TGCTGTCCGGATACACACGCACGCACACATGCAGATATGCTGCCTGGGCACACACTTCCGGA
 CACACATGCACACACAGGTGCAGATATGCTGCCTGGACACACGCAGACTGACGTGCTTTTGG
 GAGGGTGTGCCGTGAAGCCTGCAGTACGTGTCCGTGAGGCTCATAGTTGATGAGGGACTTT
 CCCTGCTCCACCGTCACTCCCCCAACTCTGCCCGCCTCTGTCCCCGCCTCAGTCCCCGCCTC
 CATCCCCGCCTCTGTCCCCTGGCCTTGGCGGCTATTTTTGCCACCTGCCTTGGGTGCCCAGG
 AGTCCCCTACTGCTGTGGGCTGGGGTTGGGGGACAGCAGCCCCAAGCCTGAGAGGCTGGAG
 CCCATGGCTAGTGGCTCATCCCAGTGCACTTCCCCTTGACACAGAGAAGGGGCTTGGTA
 TTTATATTTAAGAAATGAAGATAATATTAATAATGATGGAAGGAAGACTGGGTTGCAGGGAC
 TGTGGTCTCTCCTGGGGCCCCGGGACCCGCTGGTCTTTCAGCCATGCTGATGACCACACCCC
 GTCCAGGCCAGACACCACCCCCACCCCACTGTCGTGGTGGCCCCAGATCTCTGTAATTTTA
 TGTAGAGTTTGAGCTGAAGCCCCGTATATTTAATTTATTTTGTAAACACAAAA

FIGURE 70

MTPSPLLLLLLPLLLLGAFPPAAAARGPPKMADKVVPQVARLGRTVRLQCPVEGDPPPLTM
WTKDGRTIHSGWSRFRVLPQGLKVKQVEREDAGVYVCKATNGFGSLSVNYTLVVLDISP
ESLGPDSSSGGQEDPASQQWARPRFTQPSKMRRRVIA R PVGSSVRLKCVASGHPRPDITWMK
DDQALTRPEAAEPRKKKWTLSLKNLRPEDSGKYTCRVSNRAGAINATYKVDVIQRTRSKPVL
TGTHPVNTTVDFGGTTSFQCKVRSDVKPVIQWLKRVEYGAEGRHNSTIDVGGQKFVVLPTGD
VWSRPDGSYLNKLLITRARQDDAGMYICLGANTMGYSFRSAFLT VLPDPKPPGPPVASSSSA
TSLPWPVVIGIPAGAVFILGTLLLWLCQAQKKPCTPAPAPPLPGHRPPGTARDRSGDKDLPS
LAALSAGPGVGLCEEHGSPAAPQHLLGPGPVAGPKLYPKLYTDIHTHTHTSHTHSHVEGKV
HQHIHYQC

FIGURE 71

CCCAGCTGAGGAGCCCTGCTCAAGACACGGTCACTGGATCTGAGAAACTTCCCAGGGGACCGCATTCCAGAGTC
 AGTGACTCTGTGAAGCACCCACATCTACCTCTTGCCACGTTCCCACGGGCTTGGGGGAAAAG**AT**GGTGGGGACCA
 AGGCTGGGTGTTCTCCTTCCCTGGTCTGGAGTCAATCTGTGTTGGGGAGACAGACGATGCTCACCCAGTCA
 GTAAGAAGAGTCCAGCCTGGGAAGAAGAACCCAGCATCTTTGCCAAGCCTGCCGACACCCTGGAGAGCCCTGG
 TGAGTGGACAACATGGTTCAACATCGACTACCCAGCGGGGAAGGGCGACTATGAGCGGCTGGACGCCATTGCT
 TCTACTATGGGGACCGTGTATGTGCCCGTCCCCGCTGCGGCTAGAGGCTCGGACCACTGACTGGACACCTGCGGGC
 AGCACTGGCCAGGTGGTCCATGGTAGTCCCCGTGAGGGTTTCTGGTGCCTCAACAGGGAGCAGCGGCCCTGGCCA
 GAACTGCTCTAATTACACCGTACGCTTCCCTGTCGCCACGAGTCCCTGCGCCGAGACACAGAGCGCATCTGGA
 GCCCATGGTCTCCCTGGAGCAAGTGTCTCAGCTGCCGTGTGGTCACTGGGGTCCAGACTCGCACACGCATTTGC
 TTGGCAGAGATGGTGTGCTGTGCAAGTGAAGGGTCAAGAGGGTCACTGCATGGGCCAGGACTGTACAGC
 CTGTGACCTGACCTGCCAATGGCCAGGTGAATGCTGACTGTGATGCTGCATGTGCCAGGACTTCATGCTTC
 ATGGGGCTGTCTCCCTTCCCGGAGGTGCCCCAGCCTCAGGGGCTGCTATCTACCTCCTGACCAAGACGCCGAAG
 CTGCTGACCCAGACAGACAGTGTATGGGAGATTCCGAATCCCTGGCTGTGCTGCTGATGGGCAAGCATCTCTGAA
 GATCACAAAGGTCAAGTTTGCCCCATTGTACTACAATGCCAAGACTAGCCTGAAGGACCCACCATCAAGG
 CAGAGTTTGTGAGGGCAGAGACTCCATACATGGTGTGAACCTGAGACAAAAGCACGGAGAGCTGGGCAGAGC
 GTGCTCTGTGCTGTAAAGGCCACAGGGAAGCCAGGCCAGCAAGTATTTTGGTATCATAATGACACATTGCT
 GGATCCTTCCCTCAAGCATGAGAGCAAGTGGTGTGAGGAACTGCAGCAGCACCAGGCTGGGGAGTACT
 TTTGCAAGGCCCAGAGTGTATGCTGGGGCTGTGAAGTCCAAGGTTGCCAGCTGATTGTACAGCATCTGATGAG
 ACTCCTTGCAACCCAGTTTCTGAGAGCTATCTTATCCGGCTGCCCATGATTGCTTTTCAAGATGCCACCACTC
 TCGGAAAGAGCCCATCACTTTGGAAGCCATGGAGACCAACATCATCCCCCTGGGGGAAGTGGTTGGTGAAGACC
 CCATGGCTGAAGTGGAGATTCCATCCAGGAGTTTCTACAGGCAGAATGGGGAGCCCTACATAGGAAAAGTGAAG
 GCCAGTGTGACCTTCCCTGGATCCCCGGAATATTTCCACAGCCACAGCTGCCAGACTGACCTGAACCTTCATCAA
 TGACGAAGGAGACACTTTCCCCCTTCGGACGTATGGCATGTTCTCTGTGGACTTCAGAGATGAGGTCACTCAG
 AGCCACTTAATGCTGGCAAAGTGAAGGTCCACCTTGACTCGACCCAGGTCAAGATGCCAGAGCACATATCCACA
 GTGAAACTCTGGTCACTCAATCCAGACACAGGGCTGTGGGAGGAGGAAGGTGATTTCAAATTTGAAAATCAAAG
 GAGGAACAAAAGAGAAGACAGAACCCTTCTGGTGGGCAACCTGGAGATTCTGTGAGAGGAGGCTCTTTAACCTGG
 ATGTTCTCTGAAAGCAGGCGGTGCTTTGTTAAGGTGAGGGCTACCGAGTGTGAGAGGTTCTTGCCTAGTGAGCAG
 ATCCAGGGGGTGTGATCTCCGTGATTAACCTGGAGCCTAGAAGTGGCTTCTTGTCCAACCTTAGGGCCTGGGG
 CCGCTTTGACAGCTGTATCACAGGGCCCAACGGGGCTGTGTGCTGCTTCTGTGATGACCATGCCCTGATG
 CCTACTCTGCCTATGTCTTGGCAAGCCTGGCTGGGGAGGAAGTGAAGCAGTGGAGTCTTCTCTAAATTCAC
 CCAATGCAATTGGCGTCCCTCAGCCCTATCTCAACAAGCTCAACTACCGTCGGACGGACCATGAGGATCCACG
 GGTAAAAAAGACAGCTTTCCAGATTAGCATGGCCAAAGCCAAAGGCCAACTCAGCTGAGGAGAGCAATGGGCCCA
 TCTATGCCTTTGAGAACCTCCGGGCATGTGAAGAGGCCACCCAGTGCAGCCCACTTCCGGTTCTACAGATT
 GAGGGGATCGATATGACTACAACACAGTCCCCTTCAACGAAGATGACCTATGAGCTGGACTGAAGACTATCT
 GGCATGGTGGCCAAAGCCGATGGAATTCAGGGCCTGCTATATCAAGGTGAAGATTGTGGGGCCACTGGAAGTGA
 ATGTGCGATCCCGCAACATGGGGGGCACTCATCGGCGGACAGTGGGGGAAGCTGTATGGAATCCGAGATTGTGAGG
 AGCACTCGGGACAGGGACCCCAATGTCTCAGTGCCTGTCTGGAGTTCAAGTGCAGTGGGATGCTCTATGA
 TCAGGACCGTGTGGACCGCACCCCTGGTGAAGGTCACTCCCCAGGGCAGCTGCCGTGAGCCAGTGTGAACCCCA
 TGCTGCATGAGTACCTGGTCAACCACTTGCCACTTGCACTCAACAACGACACCAAGTGAATACCATGCTGGCA
 CCGTTGGACCCCACTGGGCCACAACATATGGCATCTACACTGTCACTGACCAGGACCCCTCGACGGCCAAAGGAGT
 CGCGCTCGGCGCGGTGCTTTGATGGCACATCCGATGGCTCCTCCAGAATCATGAAGAGCAATGTGGGAGTAGCCC
 TCACCTTCAACTGTGTAGAGAGGCAAGTAGGCCGCCAGAGTGCTTCCAGTACCTCCAAAGCACCCAGCCAG
 TCCCCTGCTGCAGGCACTGTCCAAGGAAGAGTGCCCTCGAGGAGGCAGCAGCGAGCGAGCAGGGGTGGCCAGCG
 CCAGGGTGGAGTGGTGGCTCTCTGAGATTTCCTAGAGTTGCTCAACAGCCCCTGATCACT**TAAG**TTTTGTGGT
 ACTTACCCCTCTTCTGCCCTCATTTTCATGTGACAGCCATTGTGAGACTGATGCACAAACTGTCACTTGGTTAAT
 TTAAGCACTTCTGTTTTCTGTAATTTGCTTGTGTTTCTTTCATGCTTTTACTTACTTTTGTCCCATGCTACTGA
 TTGGCACGTGGCCCCACAATGGCACATAAAGCCCCCTTTGTGAAACTGTCTTTAAATGAAACACAAGAAAT
 GGCCACTGGTAAACTCTGCAGCTTCAACTGTACTTCATTTAATGCCATTAATGCAATATACTTCTCTCTT
 TTTGCATGGTTTTTGGCCACCTCTGCAATAGTGATAATCTGATGCTGAAGATCAAATAACCAATATAAAGCATAT
 TTCTTGGCCTTGTCTCCACAGGACATAGGCAAGCCTTGATCATAGTTTATACATATAAATGGTGGTGAATAAAG
 AAATAAAACACAATACTTTTACTTGAATGTAATAAATTAATTTATTTCTTTGCTAAATTTGGAATTTCTAGTGC
 ACATTCAAAGTTAAGCTATTAATATAGGGTGATCATAGTTCCCTCTACCAAGTCTGGAAGAACATCTCCTGGT
 ATCCACAATTACACAGGTTGCTAACTGTATTTGTACATTTCCCTTGCATTGCTTTTGTCTTGTCTAGAAAC
 CCAGTGTAGCCAGGGCAGATGTCAATAAATGCATACTCTGTATTTGAAAAA

FIGURE 72

MVGTKAWVFSFLVLEVTSLGRQTMILTQSVRRVQPGKKNPSIFAKPADTLESFGEWTTWFNFI
 DYPGGKGDIYERLDAIRFYYGDRVCARPLRLEARTTDWTPAGSTGQVVHGSPREGFWCLNREQ
 RPGQNCNSNYTVRFLCPPGSLRRDTERIWSFWSFWSKCSAACGQTGVQTRTRICLAEMVSLCS
 EASEEGQHCMGQDCTACDLTCPMGQVNADCDACMCQDFMLHGAVSLPGGAPASGAAYLLTK
 TPKLLTQTDSGGRFRIPLGLCPDGKSILKITKVKEFAPIVLTMPTSLKAATIKAEFVRAETPY
 MVMNPETKARRAGQSVSLCCKATGKPRPDKYFWYHNDTLLDPSLYKHESKLVLRLKQQHQAG
 EYFCKAQSDAGAVKSKVAQLIVTASDETPCNVPVPESYLIRLPHDCFQONATNSFYVDVGRCPV
 KTCAGQQDNGIRCRDAVQNC CGISKTEEREIQCSGYTLPTKVAKECSCQRCTETRSIVRGRV
 SAADNGEPMRFGHVYMGNSRVSMGTGYKGTFTLHVPQDTERLVLTFVDRLQKFVNTTKVLPFN
 KKGSAVFHEIKMLRRKEPITLEAMETNIIPLGEVVGEDPMAELEIPSRSFYRQNGEPYIGKV
 KASVTFLDPRNISTATAAQTDLNFINDEGDTFPLRITYGMFSVDFRDEVTSEPLNAGKVKVHL
 DSTQVKMPEHIISTVKLWSLNPDTGLWEEEGDFKFENQRRNKRDRFTFLVGNLEIRERRLFNL
 DVPESRRCFVKVRAYRSEFPLPSEQIQGVVISVINLEPRTGFLSNPRAWGRFDSVITGPNGA
 CVPAFCDQSPDAYSAYVLASLAGEELQAVESSPKFNPNAIGVPQPYLNKLNRYRRTDHEDPR
 VKKTAFQISMAKPRPNSAEESNGPIYAFENLRACEEAPPSAAHFRFYQIEGDRYDYNTPVFN
 EDDPMSWTE DYLAWWPKPMEFRACYIKVKIVGPLEVNVRSRNMGGTHRRTVGKLYGIRDVRS
 TRDRDQPNVSAACLEFKCSGMLYDQDRVDRTL VKVI PQGSCRASVNPM LHEYLVNHLPLAV
 NNDTSEYTMLAPLDPLGHNYGIYTVTDQDPRTAKEIALGRCFDGTSDGSSRIMKSNVGVALT
 FNCVERQVGRQSAFQYLQSTPAQSPAAGTVQGRVPSRRQQRASRGGQRQGGVVASLRFPRVA
 QQPLIN

FIGURE 73

CTGCAAGTTGTTAACGCCTAACACACAAGTATGTTAGGCTTCCACCAAAGTCCTCAATATACCTGAATACGCAC
 AATATCTTAACTCTTCATATTTGGTTTTGGGATCTGCTTTGAGGTCCCATCTTCATTTAAAAAAAATACAGAG
 ACCTACCTACCCGTACGCATACATACATATGTGTATATATATGTAACTAGACAAAGATCGCAGATCATAAAAGC
 AAGCTCTGCTTTAGTTTTCCAAGAAGATTACAAAGAATTTAGAGATGCTATTTGTCAAGATCCCTGTGATTCATG
 CCCTTTGGGTTACGGTGTCTCAGTGATGCAGCCCTACCCTTTGGTTTGGGGACATTATGATTTGTGTAAGACT
 CAGATTTACACGGAAGAAGGAAAGTTTGGGATTACATGGCCTGCCAGCCGGAATCCACGGACATGACAAAATA
 TCTGAAAGTGAAACTCGATCCTCCGGATATTACCTGTGGAGACCCTCCTGAGACGTTCTGTGCAATGGGCAATC
 CCTACATGTGCAATAATGAGTGTGATGCGAGTACCCCTGAGCTGGCACACCCCCCTGAGCTGATGTTTGATTTT
 GAAGGAAGACATCCCTCCACATTTTGGCAGTCTGCCACTTGGGAAGGAGTATCCCAAGCCTCTCCAGGTTAACAT
 CACTCTGTCTTGGAGCAAAACCATTTGAGCTAACAGACAACATAGTTATTACCTTTGAATCTGGGCGTCCAGACC
 AAATGATCCTGGAGAAGTCTCTCGATTATGGACGAACATGGCAGCCCTATCAGTATTATGCCACAGACTGCTTA
 GATGCTTTTTCATGATGCTAAATCCGTGAAGGATTTATCACAGCATACGGTCTTAGAAATCATTTCACAGAGA
 AGAGTACTCAACAGGGTATACAACAAATAGCAAAATAATCCACTTTGAAATCAAAGACAGGTTTCGCGCTTTTGT
 CTGGACCTCGCCTACGCAATATGGCTTCCCTCTACGGACAGCTGGATACAACCAAGAAACTCAGAGATTTCTTT
 ACAGTCACAGACCTGAGGATAAGGCTGTAAAGACCAGCCGTTGGGGAAATATTTGTAGATGAGCTACACTTGGC
 ACGCTACTTTTACGCGATCTCAGACATAAAGGTGCGAGGAAGGTGCAAGTGTAACTCTCCATGCCACTGTATGTG
 TGTATGACAACAGCAAATTGACATGCGAATGTGAGCACAACACTACAGGTCCAGACTGTGGGAAATGCAAGAAG
 AATTATCAGGGCCGACCTTGGAGTCCAGGCTCCTATCTCCCATCCCCAAAGGCACTGCAATACCTGTATCCC
 CAGTATTTCCAGTATTGGTACGAATGTCTGCGACAACGAGCTCCTGCACTGCCAGAACGGAGGGACGTGCCACA
 ACAACGTGCGCTGCTGTGCCCGGCCCATACAGGGCATCCTCTGCGAGAAGCTGCGGTGCGAGGAGGCTGGC
 AGCTGCGGCTCCGACTCTGGCCAGGGCGCGCCCCCGCACGGCACCCAGCGCTGCTGCTGCTGACACGCTGCT
 GGGAACCGCCAGCCCCCTGGTGTCTAGGTGTCACTCCAGCCACACCGGACGGGCTGTGCCGTGGGGAAAGCA
 GACACAACCCAAACATTTGCTACTAACATAGGAAACACACATACAGACACCCCCACTCAGACAGTGTACAAA
 CTAAGAAGGCCTAACTGAACCTAAGCCATATTTATCACCCGTGGACAGCACATCCGAGTCAAGACTGTAAATTC
 TGACTCCAGAGGAGTTGGCAGCTGTTGATATTATCACTGCAAATCACATTGCCAGCTGCAGAGCATATTGTGGA
 TTGGAAAGGCTGCGACAGCCCCCAACAGGAAAGACAAAAACAACAAATCAACCGACCTAAAAACATTGGC
 TACTCTAGCGTGGTGCGCCCTAGTACGACTCCGCCAGTGTGTGGACCAACCAATAGCATTCTTTGCTGTGAG
 GTGCATTGTGGGCATAAGGAAATCTGTTACAAGCTGCCATATTGGCCTGCTTCCGTCCCTGAATCCCTTCCAAC
 CTGTGCTTTAGTGAACGTTGCTCTGTAACCTCGTTGGTTGAAAGATTTCTTTGTCTGATGTTAGTGATGCACA
 TGTGTAACAGCCCCCTCTAAAAGCGCAAGCCAGTCATACCCCTGTATATCTTAGCAGCACTGAGTCCAGTGCGA
 GCACACACCCACTATACAAGAGTGGCTATAGGAAAAAAGAAAGTGTATCTATCCTTTTGTATTCAAATGAAGTT
 ATTTTCTTGAACCTACTGTAATATGTAGATTTTTTGTATTATTGCCAATTTGTGTTACCAGACAATCTGTTAAT
 GTATCTAATTCGAATCAGCAAAGACTGACATTTTATTTTGTCTCTTTTCGTTCTGTTTTGTTTCACTGTGCAGA
 GATTTCTCTGTAAGGGCAACGAACGTGCTGGCATCAAAGAATATCAGTTTACATATATAACAAGTGTAAATAAGA
 TTCCACCAAAGGACATTCTAAATGTTTTCTTGTGCTTTAACACTGGAAGATTTAAAGAATAAAAACTCCTGCA
 TAAACGATTTTCAAGGATTTGTATTGCAATTTCTTAAGATGAAAGGAACAGCCACCAAGCAGTTTCACTCACT
 TTAATGATTTCTGTGTGGACTGAGTACATTACGCTGACGAATTTAGTTCCAGGAAGATGGATTGATGTTCACT
 AGCTTGGACAACCTCTGCAAAATATGAGACTATTTCCACTTGGGAAAAATTACAACAGCAAAAAAAAAAAAAA
 AAAAAA

FIGURE 74

MYLSRSLSIHALWVTVSSVMQPYPLVWGHYDLCKTQIYTEEGKVWDYMACQPESTDMTKYLK
VKLDPPDITCGDPPETFCAMGNPYMCNNECDASTPELAHPPELMFDFEGRHPSTFWQSATWK
EYPKPLQVNITLSWSKTIELTDNIVITFESGRPDQMILEKSLDYGRTWQPYQYYATDCLDAF
HMDPKSVKDLSQHTVLEIICTEEYSTGYTTNSKIIHFEIKDRFALFAGPRLRNMASLYGQLD
TTKKLRDFFTVDLRIRLLRPAVGEIFVDELHLARYFYAISDIKVRGRCKCNLHATVCVYDN
SKLTCECEHNTTGPDCGKCKKNYQGRPWSPGSYLPIPKGTANTCIPSISSIGTNVCDNELLH
CQNGGTCHNNVRCLCPAAYTGILCEKLRCEEAGSCGSDSGQGAPPHGTPALLLLTTLLGTAS
PLVF

FIGURE 75

CCACACGCGTCCGGGTGACCTGGGCCGAGCCCTCCCGGTACGGCTAAGATTGCTGAGGAGGCGG
CGGGTAGCTGGCAGGCGCCGACTTCCGAAGGCCGCGTCCGGGCGAGGTGTCCTCATGACTT
CTCTTGTGGACC**ATG**TCCGTGATCTTTTTTGCCTGCGTGGTACGGGTAAGGGATGGACTGCC
CCTCTCAGCCTCTACTGATTTTTTACCACACCCAAGATTTTTTGGGAATGGAGGAGACGGCTCA
AGAGTTTAGCCTTGCGACTGGCCCAGTATCCAGGTCGAGGTTCTGCAGAAGGTTGTGACTTT
AGTATACATTTTTTCTTCTTTCGGGGACGTGGCCTGCATGGCTATCTGCTCCTGCCAGTGTCC
AGCAGCCATGGCCTTCTGCTTCCTGGAGACCCTGTGGTGGGAATTCACAGCTTCCTATGACA
CTACCTGCATTGGCCTAGCCTCCAGGCCATACGCTTTTCTTGAGTTTGACAGCATCATTCAG
AAAGTGAAGTGGCATTTTAACTATGTAAGTTCCTCTCAGATGGAGTGCAGCTTGGAATAAAT
TCAGGAGGAGCTCAAGTTGCAGCCTCCAGCGGTTCTCACTCTGGAGGACACAGATGTGGCAA
ATGGGGTGATGAATGGTCACACACCGATGCACTTGGAGCCTGCTCCTAATTTCCGAATGGAA
CCAGTGACAGCCCTGGGTATCCTCTCCCTCATTCTCAACATCATGTGTGCTGCCCTGAATCT
CATTCGAGGAGTTCACCTTGCGAACAATTCTTTACAGGATCCAAGGAGCTGGTTCTGCTGGT
TGGACCAAACCTCG**TGA**GCCAGCCACCCCTGACCCAAATGAGGAGAGCTCTGATTCTCCCAT
CCGGGAGCAGTGATGTCAAACCTTCTGCTGCTGGGGAAATCTCATCAGCAGGGAGCCTGTGGA
AAAGGGCATGTGAGTGAATCTGGGAATGGCTGGATTTCGAAACATCTGCCCATGTGTATTG
ATGGCAGAGCTGTTGCCACAAAGCGCCTTTTATTTAGGGTAAAATTAACAAATCCATTCTAT
TCCTCTGACCCATGCTTAGTACATATGACCTTTAACCCTTACATTTATATGATTCTGGGGTT
GCTTCAGAAGTGTTATTTTCATGAATCATTCATATGATTTGATCCCCAGGATTCTATTTTGT
TTAATGGGCTTTTCTACTAAAAGCATAAAATACTGAGGCTGATTTAGTCAGGGCAAACCAT
TTACTTTACATATTCGTTTTTCAATACTTGCTGTTTCATGTTACACAAGCTTCTTACGGTTTTTC
TTGTAACAATAAATATTTTTGAGTAAATAATGGGTACATTTTAACAAACTCAGTAGTACAACC
TAAACTTGTATAAAAGTGTGTAAAAATGTATAGCCATTTATATCCTATGTATAAATTAAATG
AGGTGGCTTCAGAAATGGCAGAATAAATCTAAAGTGTTTATTAAAAA
AAAAG

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FIGURE 76

MSVIFFACVVRVRDGLPLSASTDFYHTQDFLEWRRRLKSLALRLAQYPGRGSAEGCDFS IHF
SSFGDVACMAICSCQCPAAMAFCFLETLWWEFTASYDTTCIGLASRPYAFLEFDSIIQKVW
HFNYVSSSQMECSLEKIQEELKLQPPAVLTLEDTDVANGVMNGHTPMHLEPAPNFRMEPVTA
LGILSLILNIMCAALNLIRGVHLAEHSLQDPRSWFCWLDQTS

"ESTT" TSTT660

FIGURE 77

TGCTTCCTGGAGACCTGTGGTGGGAATTCACAGCTTCNTATGACACTACCTGCATTGGCNT
AGCCTCCAGGCCATACGCTTTTCTTGAGTTTGACAGCATCATT CAGAAAGTGAAGTGGCATT
TTAACTATGTAAGTTCCTNTCAGATGGAGTGCAGCTTGGA AAAAATTCAGGAGGAGCTCAAG
TTGCAGCCTCCAGCGGTTCTCANTATGGAGGACACAGATGTGGCAAATGGGGT

[illegible]

CTCAGCGGCGCTTCCTCGTAGCGAGCCTAGTGGCGGGTGTTTGCATTGAAACGTGAGCGCGA
 CCCGACCTTAAAGAGTGGGGAGCAAAGGGAGGACAGAGCCCTTTAAACAGAGGCGGGTGGTG
 CCTGCCCCCTTTAAGGGCGGGGCGTCCGGACGACTGTATCTGAGCCCCAGACTGCCCGAGTT
 TCTGTGCGAGGCTGCGAGGAAAGGCCCTAGGCTGGGTCTGGGTGCTTGCGGGCGGCGGCTT
 CCTCCCCGCTCGTCCCTCCCCGGGCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGTA
TGGAAGCACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCCACGAGAGGATCCGC
 GAGTGTATTATATCAACACTTCTGTTTGCAACACTGTACATCCTCTGCCACATCTTCCTGAC
 CCGCTTCAAGAAGCCTGCTGAGTTCACCACAGTGGATGATGAAGATGCCACCGTCAACAAGA
 TTGCGCTCGAGCTGTGCACCTTTACCCTGGCAATTGCCCTGGGTGCTGTCTCCTGCTCCTGCC
 TTCTCCATCATCAGCAATGAGGTGCTGCTCTCCCTGCCTCGGAACACTACATCCAGTGGCT
 CAACGGCTCCCTCATCCATGGCCTCTGGAACCTTGTTTTTCTCTTCCCCAACCTGTCCCTCA
 TCTTCCTCATGCCCTTTGCATATTTCTTCACTGAGTCTGAGGGCTTTGCTGGCTCCAGAAAG
 GGTGTCTTGGGCCGGGTCTATGAGACAGTGGTGATGTTGATGCTCCTCCTCACTCTGCTGGTGCT
 AGGTATGGTGTGGGTGGCATCAGCCATTGTGGACAAGAACAAGGCCAACAGAGAGTCACTCT
 ATGACTTTTGGGAGTACTATCTCCCCTACCTCTACTCATGCACTCTCCTTCCTTGGGGTTCTG
 CTGCTCCTGGTGTGTACTCCACTGGGTCTCGCCCGCATGTTCTCCGTCACTGGGAAGCTGCT
 AGTCAAGCCCCGGCTGCTGGAAGACCTGGAGGAGCAGCTGTACTGCTCAGCCTTTGAGGAGG
 CAGCCCTGACCCGCAGGATCTGTAATCCTACTTCCTGCTGGCTGCCTTTAGACATGGAGCTG
 CTACACAGACAGGTCTCTGGCTCTGCAGACACAGAGGGTCCTGCTGGAGAAGAGGCGGAAGGC
 TTCAGCCTGGCAACGGAACCTGGGCTACCCCCCTGGCTATGCTGTGCTTGCTGGTGCTGACGG
 GCCTGTCTGTGCTCATTGTGGCCATCCACATCCTGGAGCTGCTCATCGATGAGGCTGCCATG
 CCCCAGGCATGCAGGGTACCTCCTTAGGCCAGGTCTCCTTCTCCAAGCTGGGCTCCTTTGG
 TGCCGTCAATTCAAGTTGTACTCATCTTTTACCTAATGGTGTCTCAGTTGTGGGCTTCTATA
 GCTCTCACTCTTCCGGAGCCTGCGGCCCAGATGGCACGACACTGCCATGACGCAGATAATT
 GGAACACTGTGTCTGTCTCCTGGTCCCTAAGCTCAGCACTTCCTGTCTTCTCTCGAACCCTGGG
 GCTCACTCGCTTTGACCTGCTGGGTGACTTTGGACGCTTCAACTGGCTGGGCAATTTCTACA
 TTGTGTTCTCTACAAACGCAGCCTTTGCAGGCCTCACCACACTCTGTCTGGTGAAGACCTTC
 ACTGCAGCTGTGCGGGCAGAGCTGATCCGGGCCCTTTGGGCTGGACAGACTGCCGCTGCCCGT
 CTCCGGTTTCCCCCAGGCATCTAGGAAGACCCAGCACCACTGACCTCCAGCTGGGGGTGGGA
 AGGAAAAAACTGGACACTGCCATCTGCTGCCTAGGCCTGGAGGGAAGCCCAAGGCTACTTGG
 ACCTCAGGACCTGGAATCTGAGAGGGTGGGTGGCAGAGGGGAGCAGAGCCATCTGCACTATT
 GCATAATCTGAGCCAGAGTTTGGGACCAGGACCTCCTGCTTTTCCATACTTAACTGTGGCCT
 CAGCATGGGGTAGGGCTGGGTGACTGGGTCTAGCCCCTGATCCCAAATCTGTTTACACATCA
 ATCTGCCTCACTGCTGTTCTGGGCCATCCCCATAGCCATGTTTACATGATTTGATGTGCAAT
 AGGGTGGGGTAGGGGCAGGGAAAGGACTGGGCCAGGGCAGGCTCGGGAGATAGATTGTCTCC
 CTTGCCTCTGGCCCAGCAGAGCCTAAGCACTGTGCTATCCTGGAGGGGGCTTTGGACCACCTG
 AAAGACCAAGGGGATAGGGAGGAGGAGGCTTCAGCCATCAGCAATAAAGTTGATCCAGGGA
 AAAAAA

FIGURE 79

MEAPDYEVL SVREQLFHERIRECIISTLLFATLYILCHIFLTRFKKPAEFTTVDDDEDATV NK
IALELCTFTLAIALGAVLLLPFSIISNEVLLSLPRNYIIQWLNGSLIHGLWNLVFLFPNLSL
IFLMPFAYFFTESEGFAGSRKGV LGRVYETVVMLMLLTLLVLGMVWVASAIVDKNKANRESL
YDFWEYYLPYLYSCISFLGVLLLLVCTPLGLARMFSVTGKLLVKPRLLEDLEEQLYCSAFEE
AALTRRICNPTSCWLPLDMELLHRQVLALQTQRVLLEKRRKASAWQRNLGYPLAMLCLLVLT
GLSVLIVAIHILELLIDEAAMP RGMQGTSLGQVSFSKLGSFGAVIQVVLIFYLMVSSVVG FY
SSPLFRSLRPRWHD TMTQIIIGNCVCLLVLSALPVFSRTLGLTRFDLLGDFGRFNWLG N FY
IVFLYNAAFAGLTTLCLVKTF TAAVRAELIRAFGLDRLPLPVSGFPQASRKTQH Q

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FIGURE 80

GGCTGCCGAGGGAAGGCCCTTGGGTGGTCTTGGTTGCTTGGCGGCGGCGGNTTCNTCCCC
GCTCGTCCTCCCCGGGCCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGTATGGAAGC
ACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCCACGAGAGGATCCGCGAGTGTA
TTATATCAACACTTCTGTTTGCAACACTGTACATCCTCTGCCACATCTTCCTGACCCGCTTC
AAGAAGCCTGCTGAGTTCACCACAGTGGATGATGAAGATGCCACCG

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FIGURE 81

GACCGACCTTAAAGAGTGGGAGCAAAGGGAGGACAGAGCCTTTTAAAACGAGGCGGTGGTGC
CTGCCCTTTAAGGGCGGGGCGTCCGGACGACTGTATCTGAGCCCCAGACTGCCCCGAGTTTC
TGTCGCAGGCTGCGAGGAAAGGCCCTAGGCTGGGTCTGGTGCTTGGCGGCGGCGGCTTCCT
CCCCGTTGTCNTCCCCGGGCCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGTATGGA
AGCACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCCACGAGAGGATCCGCGAGT
GTATTATATCAACACTTCTGTTTGCAACACTGTACATCNTCTGCCACATCTTCCTGACCCGC
TTCAAGAAGCCTGCTGAGTTCACCACAGTGGATGATGAAGATGCCACCGTCAACAAGATTGC
GCTCGAGCTGTGCACCTTTACCCTGGCAATTGCCCTGGGTGCTGTCCTGCTCCTGCCCTTCT
CCATCATCAGCAATGAGGTGCTGCACTCCC

TGGT "TGTGGG"

FIGURE 82

GATGTGCTCCTTGGAGCTGGTGTGCAGTGTCTGACTGTAAGATCAAGTCCAAACCTGTTTT
GGAATTGAGGAACTTCTCTTTTGATCTCAGCCCTTGGTGGTCCAGGTCTTC**ATG**CTGCTGT
GGGTGATATTACTGGTCCTGGCTCCTGTCAGTGGACAGTTTGCAAGGACACCCAGGCCCAT
ATTTTCCTCCAGCCTCCATGGACCACAGTCTTCCAAGGAGAGAGAGTGACCCTCACTTGCAA
GGGATTTGCTTCTACTCACCACAGAAAACAAAATGGTACCATCGGTACCTTGGGAAAGAAA
TACTAAGAGAAACCCAGACAATATCCTTGAGGTTAGGAATCTGGAGAGTACAGATGCCAG
GCCCAGGGCTCCCCTCTCAGTAGCCCTGTGCACTTGGATTTTTCTTCAGAGATGGGATTTCC
TCATGCTGCCCAGGCTAATGTTGAACTCCTGGGCTCAAGTGATCTGCTCACCT**TAG**GCCTCTC
AAAGCGCTGGGATTACAGCTTCGCTGATCCTGCAAGCTCCACTTTCTGTGTTTGAAGGAGAC
TCTGTGGTTCTGAGGTGCCGGGCAAAGGCGGAAGTAACACTGAATAATACTATTTACAAGAA
TGATAATGTCCTGGCATTCTTAATAAAAGAACTGACTTCCAAAAAAAAAAAAAAAAAAAAA
AAA

[illegible]

MLLWVILLVLAPVSGQFARTPRPIIFLQPPWTTVFQGERVTLTCKGFRFYSPQKTKWYHRYL
GKEILRETPDNILEVQESGEYRCQAQGSPLSSPVHLDFSSEMGFPHAAQANVELLGSSDLLT

FIGURE 84

CAGAAGAGGGGGCTAGCTAGCTGTCTCTGCGGACCAGGGAGACCCCCGCGCCCCCCCCGGTGT
 GAGGCGGCCTCACAGGGCCGGGTGGGCTGGCGAGCCGACGCGGCGGCGGAGGAGGCTGTGAG
 GAGTGTGTGGAACAGGACCCGGGACAGAGGAACCCATGGCTCCGCAGAACCTGAGCACCTTTT
 GCCTGTTGCTGCTATACCTCATCGGGGCGGTGATTGCCGGACGAGATTTCTATAAGATCTTG
 GGGGTGCCTCGAAGTGCCTCTATAAAGGATATTAAAAAGGCCTATAGGAACTAGCCCTGCA
 GCTTCATCCCGACCGGAACCCTGATGATCCACAAGCCCAGGAGAAATTCCAGGATCTGGGTG
 CTGCTTATGAGGTTCTGTGAGATAGTGAGAAACGGAAACAGTACGATACTTATGGTGAAGAA
 GGATTAAAAGATGGTCATCAGAGCTCCCATGGAGACATTTTTTTCACACTTCTTTGGGGATTT
 TGGTTTCATGTTTGGAGGAACCCCTCGTCAGCAAGACAGAAATATTCCAAGAGGAAGTGATA
 TTATTGTAGATCTAGAAGTCACTTTGGAAGAAGTATATGCAGGAAATTTTGTGGAAGTAGTT
 AGAAACAAACCTGTGGCAAGGCAGGCTCCTGGCAAACGGAAGTGCAATTGTGCGCAAGAGAT
 GCGGACCACCCAGCTGGGCCCTGGGCGCTTCCAAATGACCCAGGAGGTGGTCTGCGACGAAT
 GCCCTAATGTCAAACCTAGTGAATGAAGAACGAACGCTGGAAGTAGAAATAGAGCCTGGGGTG
 AGAGACGGCATGGAGTACCCCTTTATTGGAGAAGGTGAGCCTCACGTGGATGGGGAGCCTGG
 AGATTTACGGTTCCGAATCAAAGTTGTCAAGCACCCAATATTTGAAAGGAGAGGAGATGATT
 TGTACACAAATGTGACAATCTCATTAGTTGAGTCACTGGTTGGCTTTGAGATGGATATTACT
 CACTTGGATGGTCACAAGGTACATATTTCCCGGGATAAGATCACCAGGCCAGGAGCGAAGCT
 ATGGAAGAAAGGGGAAGGGCTCCCCAACTTTGACAACAACAATATCAAGGGCTCTTTGATAA
 TCACCTTTTGATGTGGATTTTCCAAAAGAACAGTTAACAGAGGAAGCGAGAGAAGGTATCAAA
 CAGCTACTGAAACAAGGGTCAGTGCAGAAGGTATACAATGGACTGCAAGGATATTGAGAGTG
 AATAAAATTGGACTTTGTTTTAAATAAGTGAATAAGCGATATTTATTATCTGCAAGGTTTTT
 TTGTGTGTGTTTTTGTTTTTATTTTCAATATGCAAGTTAGGCTTAATTTTTTTTATCTAATGA
 TCATCATGAAATGAATAAGAGGGCTTAAGAATTTGTCCATTTGCATTTCGAAAAGAATGACC
 AGCAAAAGGTTTACTAATACCTCTCCCTTTGGGGATTTAATGTCTGGTGCTGCCGCCTGAGT
 TTCAAGAATTAAAGCTGCAAGAGGACTCCAGGAGCAAAAGAAACACAATATAGAGGGTTGGA
 GTTGTTAGCAATTTCAATCAAAATGCCAACTGGAGAAGTCTGTTTTTAAATACATTTTGTG
 TTATTTTAA

FIGURE 85

MAPQNLSTFCLLLLYLIGAVIAGRDFYKILGVPRASIKDIKKAYRKLALQLHPDRNPDDPQ
AQEKFQDLGAAYEVLSDSEKRKQYDTYGEGLKDGHQSSHGDI FSHFFGDFGMFGGTPRQQ
DRNI PRGSDI IVDLEVTLEEYAGNFVEVVRNKPVARQAPGKRKCNCRQEMRTTQLGPGRFQ
MTQEVVCD ECPNVKLVNEERTLEVEIEPGVRDGM EYPFFIGEGEPHVDGEPGDLRFRIKVVKH
PIFERRGDDLYTNVTISLVESLVGFEMDITHLDGHKVHISRDKITRPGAKLWKKGEGLPNFD
NNNIKGS LIITFDVDFPKEQLTEEAREGIKQLLKQGSVQKVYNGLOGY

Important features:

Signal peptide:

amino acids 1-22

Cell attachment sequence.

amino acids 254-257

Nt-dnaJ domain signature.

amino acids 67-87

Homologous region to Nt-dnaJ domain proteins.

amino acids 26-58

N-glycosylation site.

amino acids 5-9, 261-265

Tyrosine kinase phosphorylation site.

amino acids 253-260

N-myristoylation site.

amino acids 18-24, 31-37, 93-99, 215-221

Amidation site.

amino acids 164-168

FIGURE 86

TGGGACCAGGGAACCCCGGGCCCCCGGTGGAGNGCCTAACAGGCCGGTGGNTGCGACCGAA
GCGGCGGGCGGAGGAGGTTTTGAGGATTTTGGAAACAGGACCCGGACAGAGGAACCATGGTT
CCGCAGAACNTGAGCACNTTTTGCCTGTTGNTGNTATACTTCATCGGGGCGGTGATTGCCGG
ACGAGATTTNTATAAGATTTTGGGGTGCCTNAGAAGTGCCTTNTATAAAGGATATTAAAAAGG
CCTATAGGAAACTAGCCCTGCAGNTTATCCCGACCGGAACCCTGATGATCCACAAGCCCAG
GAGAAATTCAGGATTTGGGTGCTGCTTATGAGGTTNTGTCAGATAGTGAGAAACGGAAACA
GTACGATAATTATGGTGAAGAAGGATTAAAAGATGGTNATCAGAGCTCCCATGGAGACATTT
TTTCACACTTNTTTGGGGATTTTGGTTTCATGTTTGGAGGAACCCCTNGTCAGCAAGACAGA
AATATTCCAAGAG

FIGURE 87

GGCACGAGGCGGCGGGGCAGTCGCGGGATGCGCCCGGGAGCCACAGCCTGAGGCCCTCAGGT
CTCTGCAGGTGTCGTGGAGGAACCTAGCACCTGCCATCCTCTTCCCCAATTTGCCACTTCCA
GCAGCTTTAGCCCATGAGGAGGATGTGACCGGGACTGAGTCAGGAGCCCTCTGGAAGC**ATGG**
AGACTGTGGTGATTGTTGCCATAGGTGTGCTGGCCACCATCTTTCTGGCTTCGTTTGCAGCC
TTGGTGCTGGTTTGCAGGCAGCGCTACTGCCGGCCGCGAGACCTGCTGCAGCGCTATGATTC
TAAGCCCATTTGTGGACCTCATTGGTGCCATGGAGACCCAGTCTGAGCCCTCTGAGTTAGAAC
TGGACGATGTCGTTATCACCAACCCCCACATTGAGGCCATTCTGGAGAATGAAGACTGGATC
GAAGATGCCTCGGGTCTCATGTCCCACTGCATTGCCATCTTGAAGATTTGTCACACTCTGAC
AGAGAAGCTTGTTGCCATGACAATGGGCTCTGGGGCCAAGATGAAGACTTCAGCCAGTGTCA
GCGACATCATTGTGGTGGCCAAGCGGATCAGCCCCAGGGTGGATGATGTTGTGAAGTCGATG
TACCCTCCGTTGGACCCCAAACCTCTGGACGCACGGACGACTGCCCTGCTCCTGTCTGTCTAG
TCACCTGGTGCTGGTGACAAGGAATGCCTGCCATCTGACGGGAGGCCTGGACTGGATTGACC
AGTCTCTGTGCGCTGCTGAGGAGCATTTGGAAGTCCTTCGAGAAGCAGCCCTAGCTTCTGAG
CCAGATAAAGGCCCTCCCAGGCCCTGAAGGCTTCCTGCAGGAGCAGTCTGCAATTT**TAG**GCCT
ACAGGCCAGCAGCTAGCCATGAAGGCCCTGCCGCCATCCCTGGATGGCTCAGCTTAGCCTT
CTACTTTTTCTATAGAGTTAGTTGTTCTCCACGGCTGGAGAGTTCAGCTGTGTGTGCATAG
TAAAGCAGGAGATCCCCGTCAGTTTATGCCTCTTTTGCAGTTGCAAACCTGTGGCTGGTGAGT
GGCAGTCTAATACTACAGTTAGGGGAGATGCCATTCACTCTCTGCAAGAGGAGTATTGAAAA
CTGGTGGACTGTCAGCTTTATTTAGCTCACCTAGTGTTTTCAAGAAAATTGAGCCACCGTCT
AAGAAATCAAGAGGTTTACATTAAAATTAGAATTTCTGGCCTCTCTCGATCGGTCAGAATG
TGTGGCAATTCTGATCTGCATTTTTCAGAAGAGGACAATCAATTGAAACTAAGTAGGGGTTTC
TTCTTTTGGCAAGACTTGTAATCTCTCACCTGGCCTGTTTCATTTATTTGTATTATCTGCCT
GGTCCCTGAGGCGTCTGGGTCTCTCCTCTCCCTTGCAAGTTTGGGTTTGAAGCTGAGGAACT
ACAAAGTTGATGATTTCTTTTTTATCTTTATGCCTGCAATTTTACCTAGCTACCACTAGGTG
GATAGTAAATTTATACTTATGTTTCCCTCAAAAAAAAAAAAAA

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FIGURE 88

METVVIVAIGVLATIFLASFAALVLVCRQRYCRPRDLLQRYDSKPIVDLIGAMETQSEPSEL
ELDDVVITNPHIEAILENEDWIEDASGLMSHCIAILKICHTLTEKLVAMTMGSGAKMKT SAS
VSDIIVVAKRISPRVDDVVKSMYPPLDPKLLDARTTALLSVSHLVLVTRNACHLTGGLDWI
DQSLSAAEEHLEVLREAALASEPDKGLPGPEGFLQEQSAI

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GCTTCATTTCTCCCGACTCAGCTTCCCACCCCTGGGCTTTC CGAGGTGCTTTCGCCGCTGTCC
CCACCACTGCAGCC**ATG**ATCTCCTTAACGGACACGCAGAAAATTGGAATGGGATTAACAGGA
TTTGAGTGTTCCTGTTCTTTGGAATGATTCTCTTTTTTGACAAAGCACTACTGGCTAT
TGGAATGTTTTATTTGTAGCCGGCTTGGCTTTTGTAAATTGGTTAGAAAGAACATT CAGAT
TCTTCTTCCAAAAACATAAAATGAAAGCTACAGGTTTTTTTTCTGGGTGGTGTATTTGTAGTC
CTTATTGGTTGGCCTTTGATAGGCATGATCTTCGAAATTTATGGATTTTTTCTCTTGTT CAG
GGGCTTCTTTCCTGTCGTTGTTGGCTTTATTAGAAGAGTGCCAGTCCTTGGATCCCTCCTAAAT
TTACCTGGAATTAGATCATTTGTAGATAAAGTTGGAGAAAGCAACAATATGGTAT**TA**ACAACA
AGTGAATTTGAAGACTCATTTAAAATATTGTGTTATTTATAAAGTCATTTGAAGAATATTCA
GCACAAAATTAAATTACATGAAATAGCTTGTAATGTTCTTTACAGGAGTTTAAAACGTATAG
CCTACAAAGTACCAGCAGCAAATTAGCAAAGAAGCAGTGAAAACAGGCTTCTACTCAAGTGA
ACTAAGAAGAAGTCAGCAAGCAAAGTCTGAGAGAGGTGAAATCCATGTTAATGATGCTTAAGAA
ACTCTTGAAGGCTATTTGTGTTGTTTTTCCACAATGTGCGAAACTCAGCCATCCTTAGAGAA
CTGTGGTGCCTGTTTCTTTTCTTTTTATTTTGAAGGCTCAGGAGCATCCATAGGCATTTGCT
TTTTAGAAGTGTCCACTGCAATGGCAAAAATATTTCCAGTTGCACTGTATCTCTGGAAGTGA
TGCATGAATTCGATTGGATTGTGTCATTTTAAAGTATTAAAACCAAGGAAACCCCAATTTTG
ATGTATGGATTACTTTTTTTTTGNGCNCAGGGCC

FIGURE 90

MISLTDTQKIGMGLTGFGVFFLFFGMILFFDKALLAIGNVLFVAGLAFVIGLERTFRFFFQK
HKMKATGFFLGGVFVVLIGWPLIGMIFEIYGFFLLFRGFFPVVVGFIIRVPVLGSLLNLPGI
RSFVDKVGESNNMV

Important features:

Transmembrane domains:

amino acids 12-30 (typeII), 33-52, 69-89 and 93-109

N-myristoylation sites.

amino acids 11-16, 51-56 and 116-121

Aminoacyl-transfer RNA synthetases class-II protein.

amino acids 49-59

FIGURE 91

GAAGACGTGGCGGCTCTCGCCTGGGCTGTTTCCCGGCTTCATTTCTCCCGACTCAGCTTCCC
ACCNTGGGCTTTCCGAGGTGCTTTCGCCGCTGTCCCCACCACTGCAGCCATGATCTCCTTAA
CGGACACGCAGAAAATTGGAATGGGATTAACCGGATTGGAGTGTTTTTCCTGTTCTTTGGA
ATGATTCTCTTTTTTGACAAAGCACTACTGGCTATTGGAAATGTTTTATTTGTAGCCGGCTT
GGCTTTTGTAATTGGTTTAGAAAGAACATTCAGATTCTTCTTCCAAAAACATAAAATGAAAG
CTACAGGTTTTTTTCTGGGTGGTGTATTTGTAGTCCTTATTGGTTGGCCTTTGATAGGCATG
ATCTTCGAAATTTATGGATTTTTTCTCTTGTTT

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FIGURE 92

GGCACGAGGCTGAACCCAGCCGGCTCCATCTCAGCTTCTGGTTTCTAAGTCCATGTGCCAAA
GGCTGCCAGGAAGGAGACGCCTTCCTGAGTCCTGGATCTTTCTTCCTTCTGGAAATCTTTGA
CTGTGGGTAGTTATTTATTTCTGAATAAGAGCGTCCACGCATC**ATG**GACCTCGCGGGACTGC
TGAAGTCTCAGTTCCTGTGCCACCTGGTCTTCTGCTACGTCTTTATTGCCTCAGGGCTAATC
ATCAACACCATTTCAGCTCTTCACTCTCCTCCTCTGGCCCATTAACAAGCAGCTCTTCCGGAA
GATCAACTGCAGACTGTCCTATTGCATCTCAAGCCAGCTGGTGATGCTGCTGGAGTGGTGGT
CGGGCACGGAATGCACCATCTTCACGGACCCGCGCGCCTACCTCAAGTATGGGAAGGAAAAT
GCCATCGTGGTTCTCAACCACAAGTTTGAAATTGACTTTCTGTGTGGCTGGAGCCTGTCCGA
ACGCTTTGGGCTGTTAGGGGGCTCCAAGGTCTGGCCAAGAAAGAGCTGGCCTATGTCCCAA
TTATCGGCTGGATGTGGTACTTCACCGAGATGGTCTTCTGTTGCGCAAGTGGGAGCAGGAT
CGCAAGACGGTTGCCACCAGTTTGCAGCACCTCCGGGACTACCCCGAGAAGTATTTTTTCCT
GATTCACTGTGAGGGCACACGGTTCACGGAGAAGAAGCATGAGATCAGCATGCAGGTGGCCC
GGGCCAAGGGGCTGCCTCGCCTCAAGCATCACCTGTTGCCACGAACCAAGGGCTTCGCCATC
ACCGTGAGGAGCTTGAGAAATGTAGTTTCAGCTGTATATGACTGTACACTCAATTTTCAGAAA
TAATGAAAATCCAACACTGCTGGGAGTCTTAAACGGAAAGAAATACCATGCAGATTTGTATG
TTAGGAGGATCCCACTGGAAGACATCCCTGAAGACGATGACGAGTGCTCGGCCTGGCTGCAC
AAGCTCTACCAGGAGAAGGATGCCTTTCAGGAGGAGTACTACAGGACGGGCACCTTCCCAGA
GACGCCCATGGTGCCCCCCCCGGCGGCCCTGGACCCTCGTGAACTGGCTGTTTTGGGCCTCGC
TGGTGCTCTACCCTTTCTTCCAGTTCCTGGTCAGCATGATCAGGAGCGGGTCTTCCCTGACG
CTGGCCAGCTTCATCCTCGTCTTCTTTGTGGCCTCCGTGGGAGTTCGATGGATGATTGGTGT
GACGGAAATTGACAAGGGCTCTGCCTACGGCAACTCTGACAGCAAGCAGAACTGAATGACT**T**
GACTCAGGGAGGTGTCACCATCCGAAGGGAACCTTGGGGAACCTGGTGGCCTCTGCATATCCT
CCTTAGTGGGACACGGTGACAAAGGCTGGGTGAGCCCCTGCTGGGCACGGCGGAAGTCACGA
CCTCTCCAGCCAGGGAGTCTGGTCTCAAGCCGGATGGGGAGGAAGATGTTTTGTAATCTTT
TTTTCCCCATGTGCTTTAGTGGGCTTTGGTTTTCTTTTTGTGCGAGTGTGTGTGAGAATGGC
TGTGTGGTGAGTGTGAACTTTGTTCTGTGATCATAGAAAGGGTATTTTAGGCTGCAGGGGAG
GGCAGGGCTGGGGACCGAAGGGGACAAGTTCCCCTTTCATCCTTTGGTGCTGAGTTTTCTGT
AACCCTTGGTTGCCAGAGATAAAGTGAAAAGTGCTTTAGGTGAGATGACTAAATTATGCCTC
CAAGAAAAAAAATTAAGTGCTTTTCTGGGTCAAAAAAAAAAAAA

FIGURE 94

CTGAGGCGGCGGTAGCATGGAGGGGGAGAGTACGTCGGCGGTGCTCTCGGGCTTTGTGCTCG
 GCGCACTCGCTTTCCAGCACCTCAACACGGACTCGGACACGGAAGGTTTTCTTCTTGGGGAA
 GTAAAAGGTGAAGCCAAGAACAGCATTACTGATTCCCAAATGGATGATGTTGAAGTTGTTTA
 TACAATTGACATTCAGAAATATATTCCATGCTATCAGCTTTTTAGCTTTTATAATTCTTCAG
 GCGAAGTAAATGAGCAAGCACTGAAGAAAATATTATCAAATGTCAAAAAGAATGTGGTAGGT
 TGGTACAAATTCCGTCGTCATTTCAGATCAGATCATGACGTTTAGAGAGAGGCTGCTTCACAA
 AAAC TTGCAGGAGCATTTTTTCAAACCAAGACCTTGTTTTTCTGCTATTAACACCAAGTATAA
 TAACAGAAAGCTGCTCTACTCATCGACTGGAACATTCCTTATATAAACCTCAAAAAGGACTT
 TTTTACAGGGTACCTTTTAGTGGTTGCCAATCTGGGCATGTCTGAACAACTGGGTATATAAAC
 TGTATCAGGTTCCCTGTATGTCCACTGGTTTTAGCCGAGCAGTACAAACACACAGCTCTAAAT
 TTTTTGAAGAAGATGGATCCTTAAAGGAGGTACATAAGATAAATGAAATGTATGCTTCATTA
 CAAGAGGAATTAAAGAGTATATGCAAAAAGTGGAAGACAGTGAACAAGCAGTAGATAAACT
 AGTAAAGGATGTAAACAGATTAAACGAGAAATTGAGAAAAGGAGAGGAGCACAGATTCAGG
 CAGCAAGAGAGAAGAACATCCAAAAGACCCTCAGGAGAACATTTTTCTTTGTGTCAGGCATTA
 CGGACCTTTTTTCCAAATTCTGAATTTCTTCATTCATGTGTTATGTCTTTAAAAAATAGACA
 TGTTTCTAAAAGTAGCTGTAAC TACAACCACCATCTCGATGTAGTAGACAATCTGACCTTAA
 TGGTAGAACACACTGACATTCCTGAAGCTAGTCCAGCTAGTACACCACAAATCATTAAGCAT
 AAAGCCTTAGACTTAGATGACAGATGGCAATTCAAGAGATCTCGGTTGTTAGATACACAAGA
 CAAACGATCTAAAGCAAATACTGGTAGTAGTAACCAAGATAAAGCATCCAAAATGAGCAGCC
 CAGAAACAGATGAAGAAATTGAAAAGATGAAGGGTTTTGGTGAATATTCACGGTCTCCTACA
 TTTTTGATCCTTTTAAACCTTACAAGGAGATTTTTTTATTTGGCTGATGGGTAAAGCCAAACAT
 TTCTATTGTTTTTACTATGTTGAGCTACTTGCAGTAAGTTCATTTGTTTTTACTATGTTTAC
 CTGTTTGCAGTAATACACAGATAACTCTTAGTGCATTTACTTCACAAAGTACTTTTTTCAAAC
 ATCAGATGCTTTTTATTTCCAAACCTTTTTTTTACCTTTCACTAAGTTGTTGAGGGGAAGGCT
 TACACAGACACATTCTTTAGAATTGGAAAAGTGAGACCAGGCACAGTGGCTCACACCTGTAA
 TCCCAGCACTTAGGGAAGACAAGTCAGGAGGATTGATTGAAGCTAGGAGTTAGAGACCAGCC
 TGGGCAACGTATTGAGACCATGTCTATTAAAAAATAAAATGGAAAAGCAAGAATAGCCTTAT
 TTTCAAATATGGAAAGAAATTTATATGAAAATTTATCTGAGTCATTAAAATCTCCTTAAG
 TGATACTTTTTTTAGAAGTACATTATGGCTAGAGTTGCCAGATAAAATGCTGGATATCATGCA
 ATAAATTTGCAAAACATCATCTAAAATTTAAAAA AAAAAAAAAAAAAAAAAAAAAA

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FIGURE 95

MEGESTSAVLSGFVLGALAFQHLNTDSDTEGFLLGEVKGEAKNSITDSQMDDVEVVYTIDIQ
KYIPCYQLFSFYNSSGEVNEQALKKILSNVKKNVVGWYKFRRHSDQIMTFRERLLHKNLQEH
FSNQDLVFLLLTPSIITESCSTHRLEHSLYKPQKGLFHRVPLVVANLGMSEQLGYKTVSGSC
MSTGFSRAVQTHSSKFFEEEDGSLKEVHKINEMYASLQEELKSICKKVEDSEQAVDKLVKDVN
RLKREIEKRRGAQIQAAAREKNIQKDPQENIFLCQALRTFFPNSEFLHSCVMSLKNRHVSKSS
CNYNHHLDVVDNLTLMVEHTDIPEASPASTPQIIKHKALDLDDRWQFKRSRLLDTDKRSKA
NTGSSNQDKASKMSSPETDEEIEKMKGFGEYSRSPTF

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T095T 18T66

GGCCACAGCCGCGCGGCGGAGGGCAGAGTCAAGCCAGAGCCAGTCCAGCCGGACGAGCGGACCAGCGCAGGGCAGC
CCAAGCAGCGCGCAGCGAACGCCCGCGCGCCACACCCTCTGCGGTCCCCGCGGCGCCTGCCACCCTTCCCT
CCTTCCCCGCGTCCCCGCTCGCCGCGCAGTCAGCTTGCCGGGTTGCTGCCCCGCGAAACCCCGAGGTACCA
GCCCCGCGCCTCTGCTTCCCTGGGCGCGCGCCGCTCCACGCCCTCCTTCTCCCCCTGGCCCGCGCCTGGCAC
GGGACCGTTGCCTGACGCGAGGCCAGCTACTATTTTGCGCCGCGTCTCCTCCGCTGCTGCCTCTTTCCAC
CAACTCCAATCCTTCTCCTCCAGCTCCAATCGTCTAGTCCCCGACTCCGCGAGCCCTCGGCCGCTGCGGTAG
CGCGCTTCTCCGTCCGCTCCCAAAGGTGGGAACGCGTCCGCCCGCGCCCGCACCC**ATGG**CACGGTTCGGCTTGCC
CGCGCTTCTCTGCACCCTGGCAGTGCTCAGCGCCGCGCTGCTGGCTGCCGAGCTCAAGTCGAAAAGTTGCTCGG
AAGTGCGACGTCTTTACGTGTCAAAGGCTTCAACAAGAACGATGCCCCCTCCACGAGATCAACGGTGATCAT
TTGAAGATCTGTCCCCAGGGTTCTACCTGCTGCTCTCAAGAGATGGAGGAGAAGTACAGCCTGCAAAGTAAAGA
TGATTTCAAAGGTGTGGTCAGCGAACAGTGCATCATTTGCAAGCTGTCTTGTCTTACGTTACAAGAAGTTG
ATGAATCTTCAAAGAACTACTTGAAATTCAGAGAAATCCCTGAATGATGATGTTTGTGAAGACATGAGGCCAT
TTATACATGCAAAATCTGAGCTATTTAAAGATCTCTTCGTAGAGTTGAAACGTTACTACGTGGTGGGAAATGT
GAACCTGGAAGAAATGCTAAATGACTTCTGGGCTCGCCTCCTGGAGCGGATGTTCCGCCTGGTGAACCTCCAGT
ACCCTTTACAGATGAGTATCTGGAATGTGTGAGCAAGTATACGGAGCAGCTGAAGCCCTTCGGAGATGTCCCT
CGCAAATTGAAGCTCCAGGTTACTCGTGCTTTTGTAGCAGCCCGTACTTTTCGTCAAGGCTTAGCGGTTGCGGG
AGATGTCGTGAGCAAGGTCTCCGTGGTAAACCCACAGCCCAAGTACCCTGCCCTGTTGAAGATGATCTACT
GCTCCCACTGCGGGTCTCGTGACTGTGAAGCCATGTTACAAGTACTGCTCAAAACATCATGAGAGGCTGTTTG
GCCAACCAAGGGGATCTCGATTTTGAATGGAACAATTTATAGATGCTATGCTGATGGTGGCAGAGAGGCTAGA
GGGTCTTTTCAACATTGAATCGGTGATGGATCCCATCGATGTGAAGATTTCTGATGCTATTATGAACATGCAGG
ATAATAGTGTTCAAGTGTCTCAGAAGGTTTTCCAGGGATGTGGACCCCCCAAGCCCTCCAGCTGGACGAATT
TCTCGTTCATCTCTGAAAGTGCCCTTCAGTGCTCGCTTCAGACCACATCACCCCCAGGAACGCCCAACCCACAG
AGCTGGCAGTACTTTGGACCGACTGGTTACTGATGTTCAAGGAGAAATGAAACAGGCCAAGAAATTTCTGGTCT
CCCTTCGAGCAACGTTTGCAACGATGAGAGGATGGCTGCAGGAACCGCAATGAGGATGACTGTTGGAATGG
AAAGGCAAAAGCAGGTACCTGTTTGACAGTGACAGGAAATGGATTAGCCAACCCAGGGCAACAACCCAGAGGTCCA
GGTTGACACCAGCAAACAGACATACTGATCCTTCGTCAAATCATGGCTCTTCGAGTGATGACCAGCAAGATGA
AGAATGCATACAATGGGAACGACGTGGACTTCTTTGATATCAGTGATGAAAGTAGTGGAGAAGGAAGTGGAGT
GGCTGTGAGTATCAGCAGTGCCTTCAGAGCTTTGACTACAATGCCACTGACCATGCTGTGGGAAGAGTGCCAATGA
GAAAGCCGACAGTGCTGGTGTCCTGCTGGGCGACAGGCCCTACCTCCTCACTGTCTTCTGCATCTTGTTCCTGG
TTATGCAGAGAGAGTGGAGT**TAA**TTTCTCAAACCTCTGAGAAAAAGTGTTTCATCAAAAAGTTAAAGGCCACCAATT
ATCACTTTTCTACCATCCTAGTGACTTTGCTTTTTTAAATGAATGGACAACAATGTACAGTTTTTTACTATGTGGC
CACTGGTTTAAAGAAAGTGTGACTTTGTTTTCTCATTGATTTTTGGGAGGAAAAGGGACTGTGCATTGAGTTGGT
TCTGCTCCCCCAAACCATGTTAAACGTGGCTAACAGTGTAGGTACAGAACTATAGTTAGTTGTGCATTTGTGA
TTTTATCACTCTATTATTTGTTTGTATGTTTTTCTCATTTTCGTTTGTGGGTTTTTTTTTCCAACCTGTGATCT
CGCTTGTGTTTCTTACAAGCAAAACAGGGTCCCTTCTTGGCAGCTAACATGTACGTATTTCTGAAATATTAATA
GCTGTACAGAAAGCAGGTTTTATTTATCATGTTATCTTATTTAAAGAAAAAGGCCCAAAAGC

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FIGURE 97

MARFGLPALLCTLAVLSAALLAAELKSKSCSEVRRLYVSKGFNKNDAPLHEINGDHLKICPO
GSTCCSQEMEEKYSLQSKDDFKSVVSEQCNHLQAVFASRYKKFDEFFKELLENAEKSLNDMF
VKTYGHLYMQNSELFKDLFVELKRYVVGNVNLEEMLNDFWARLLERMFLVNSQYHFTDEY
LECVSKYTEQLKPFQDVPRKLLQVTRAFVAARTFAQGLAVAGDVVSKVSVVNPTAQCTHAL
LKMIYCSHCRGLVTVKPCYNYCSNIMRGCLANQGDLD FEWNNFIDAMLMVAERLEGPFNIES
VMDPIDVKISDAIMNMQDNSVQVSQKVFQGC GPPKPLPAGRISRSESASF SARFRPHHPEE
RPTTAAGTSLDRLVTDVKEKLKQAKKFWSSLPSNVCNDERMAAGNGNEDDCWNGKGKSRYLF
AVTGNGLANQGNNPEVQVDTSKPDILILRQIMALRVMTSKMKNAYNGNDVDFFDISDESSGE
GSGSGCEYQQCPSEFDYNATDHAGKSANEKADSAGVRPGAQAYLLTVFCILFLVMQREWR

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FIGURE 98

CTCGCCCTCAAATGGGAACGCTGGCCTGGGACTAAAGCATAGACCACCAGGCTGAGTATCCT
GACCTGAGTCATCCCCAGGGATCAGGAGCCTCCAGCAGGGAACCTTCCATTATATTCTTCAA
GCAACTTACAGCTGCACCGACAGTTGCG**ATG**AAAGTTCTAATCTCTTCCCTCCTCCTGTTGC
TGCCACTAATGCTGATGTCCATGGTCTCTAGCAGCCTGAATCCAGGGGTGCCAGAGGCCAC
AGGGACCGAGGCCAGGCTTCTAGGAGATGGCTCCAGGAAGGCGGCCAAGAATGTGAGTGCAA
AGATTGGTTCCTGAGAGCCCCGAGAAGAAAATTGATGACAGTGTCTGGGCTGCCAAAGAAGC
AGTGCCCCCTGTGATCATTTCAAGGGCAATGTGAAGAAAACAAGACACCAAAGGCACCACAGA
AAGCCAAACAAGCATTCCAGAGCCTGCCAGCAATTTCTCAAACAATGTCAGCTAAGAAGCTT
TGCTCTGCCTTTG**TAG**GAGCTCTGAGCGCCCACTCTTCCAATTAAACATTCTCAGCCAAGAA
GACAGTGAGCACACCTACCAGACACTCTTCTTCTCCACCTCACTCTCCCACTGTACCCACC
CCTAAATCATTCCAGTGCTCTCAAAAAGCATGTTTTTCAAGATCATTTTGTTTGTTGCTCTC
TCTAGTGTCTTCTTCTCTCGTCAGTCTTAGCCTGTGCCCTCCCCTTACCCAGGCTTAGGCTT
AATTACCTGAAAGATTCCAGGAAACTGTAGCTTCCTAGCTAGTGTCATTTAACCTTAAATGC
AATCAGGAAAGTAGCAAACAGAAGTCAATAAATATTTTTAAATGTCAAAAAAAAAAAAAAAAAA

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FIGURE 99

MKVLISLLLLLPLMLMSVSSSLNPGVARGHRDRGQASRRWLQEGGQECECKDWFLRAPRR
KFMTVSGLPKKQPCDHFKGNVKKTRHQRRHRKPNKHSRACQQFLKQCQLRSFALPL

10977" 7377550

FIGURE 100

AATGGCTGTCTTAGTACTTCGCCTGACAGTTGTCCTGGGACTGCTTGTCTTATTCCTGACCT
GCTATGCAGACGACAAACCAGACAAGCCAGACGACAAGCCAGACGACTCGGGCAAAGACCCA
AAGCCAGACTTCCCCAAATTCCTAAGCCTCCTGGGCACAGAGATCATTGAGAATGCAGTCGA
GTTTCATCCTCCGCTCCATGTCCAGGAGCACAGGATTTATGGAATTTGATGATAATGAAGGAA
AACATTCATCAAAGTGACATCCTCAGGACACACCCATGTGGCTCCTGGACAATCCAAGAGCA
GCCAAATCCTGCTTTTCCAGTTTGGCTCCACAAGTCCTCCAGGACAGAGCCCTCAAAGCAAC
TCCCAACGAGTTCTCAGGATTCAGGCTCTGGCTTCAACCAAACAGAACTCATTTTGAACACC
CTGACTGCATTTTTGCTTTTAGAAAGTTAGAATAAATATGGCGCTTTGGGATCACATAGTTG
ATGGAGAGGAAA

TGGTCTTTAGTACTTCGCCTGACAGTTGTCCTGGGACTGCTTGTCTTATTCCTGACCT

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FIGURE 101

MAVLVLRLTVVLGLLVFLTCYADDKPKDPDDKPDGSGKDPKPDFPKFLSLLGTEIENAVE
FILRSMRSTGFMEFDDNEGKHSSK

TOP SECRET

FIGURE 102

GGACGCCAGCGCCTGCAGAGGCTGAGCAGGGAAAAAGCCAGTGCCCCAGCGGAAGCACAGCT
CAGAGCTGGTCTGCC**ATG**GACATCCTGGTCCCCTCCTGCAGCTGCTGGTGCTGCTTCTTAC
CCTGCCCCCTGCACCTCATGGCTCTGCTGGGCTGCTGGCAGCCCCCTGTGCAAAAGCTACTTCC
CCTACCTGATGGCCGTGCTGACTCCCAAGAGCAACCGCAAGATGGAGAGCAAGAAACGGGAG
CTCTTCAGCCAGATAAAGGGGCTTACAGGAGCCTCCGGGAAAGTGGCCCTACTGGAGCTGGG
CTGCGGAACCGGAGCCAACTTTCAGTTCTACCCACCGGGCTGCAGGGTCACCTGCCTAGACC
CAAATCCCCACTTTGAGAAGTTCTTGACAAAGAGCATGGCTGAGAACAGGCACCTCCAATAT
GAGCGGTTTGTGGTGGCTCCTGGAGAGGACATGAGACAGCTGGCTGATGGCTCCATGGATGT
GGTGGTCTGCACTCTGGTGCTGTGCTCTGTGCAGAGCCCCAAGGAAGGTCTGCAGGAGGTCC
GGAGAGTACTGAGACCGGGAGGTGTGCTCTTTTTCTGGGAGCATGTGGCAGAACCATATGGA
AGCTGGGCCTTCATGTGGCAGCAAGTTTTTCGAGCCCACCTGGAAACACATTGGGGATGGCTG
CTGCCTCACCAGAGAGACCTGGAAGGATCTTGAGAACGCCAGTTCTCCGAAATCCAAATGG
AACGACAGCCCCCTCCCTTGAAGTGGCTACCTGTTGGGCCCCACATCATGGGAAAGGCTGTC
AAACAATCTTTCCCAAGCTCCAAGGCACTCATTTGCTCCTTCCCCAGCCTCCAATTAGAACA
AGCCACCCACCAGCCTATCTATCTTCCACTGAGAGGGACCT**TAG**CAGAATGAGAGAAGACATT
CATGTACCACCTACTAGTCCCTCTCTCCCCAACCTCTGCCAGGGCAATCTCTAACTTCAATC
CCGCCTTCGACAGTGAAAAAGCTCTACTTCTACGCTGACCCAGGGAGGAAACACTAGGACCC
TGTTGTATCCTCAACTGCAAGTTTCTGGACTAGTCTCCCAACGTTTGCCTCCCAATGTTGTC
CCTTTCCTTCGTTCCCATGGTAAAGCTCCTCTCGCTTTCCTCCTGAGGCTACACCCATGCGT
CTCTAGGAACTGGTCACAAAAGTCATGGTGCCTGCATCCCTGCCAAGCCCCCCTGACCCCTCT
CTCCCCACTACCACCTTCTTCCTGAGCTGGGGGCACCAGGGAGAATCAGAGATGCTGGGGAT
GCCAGAGCAAGACTCAAAGAGGCAGAGGTTTTGTTCTCAAATATTTTTTAATAAATAGACGA
AACCACG

FIGURE 103

MDILVPLLQLLVLLLTLPPLHLMALLGCWQPLCKSYFPYLMAVLTPKSNRKMESKKRELFSQL
KGLTGASGKVALLELGCGTGANFQFYPPGCRVTCCLDPNPHFEKFLTKSMAENRHLQYERFVV
APGEDMRQLADGSMDVVVCTLVLCVQSPRKVLQEVRRVLRPGGVLFWEHVAEPYGSWAFM
WQQVFEPWVKHIGDGCCLTRETWKDLENAQFSEIQMERQPPPLKWLPVGPHIMGKAVKQSF
SSKALICSFPSLQLEQATHQPIYLLPLRGT

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GTGGGATTTATTTGAGTGC AAGATCGTTTTCTCAGTGGTGGTGG AAGTTGCCTCATCGCAGG
CAGATGTTGGGGCTTTGTCCGAACAGCTCCCCTCTGCCAGCTTCTGTAGATAAGGGTTAAAA
ACTAATATTTATATGACAGAAGAAAAAGATGTCATTCCGTAAAGTAAACATCATCATCTTG
TCCTGGCTGTTGCTCTCTTCTTACTGGTTTTTGCACCATAACTTCCTCAGCTTGAGCAGTTTG
TTAAGGAATGAGGTTACAGATTCAGGAATTGTAGGGCCTCAACCTATAGACTTTGTCCCAA
TGCTCTCCGACATGCAGTAGATGGGAGACAAGAGGAGATTCCCTGTGGTCATCGCTGCATCTG
AAGACAGGCTTGGGGGGGCCATTGCAGCTATAAACAGCATT CAGCACAACTCGCTCCAAT
GTGATTTTCTACATTGTTACTCTCAACAATACAGCAGACCATCTCCGGTCTGGCTCAACAG
TGATTCCCTGAAAAGCATCAGATACAAAATTGTCAATTTTGACCCTAAACTTTTGGAAGGAA
AAGTAAAGGAGGATCCTGACCAGGGGGAATCCATGAAACCTTTAACCTTTGCAAGGTTCTAC
TTGCCAATTCTGGTTCCCAGCGCAAAGAAGGCCATATACATGGATGATGATGTAATTGTGCA
AGGTGATATTCTTGCCCTTTACAATACAGCACTGAAGCCAGGACATGCAGCTGCATTTTCAG
AAGATTGTGATT CAGCCTCTACTAAAGTTGTCATCCGTGGAGCAGGAAACCAGTACAATTAC
ATTGGCTATCTTGACTATAAAAAGGAAAGAATTCGTAAGCTTTCCATGAAAGCCAGCACTTG
CTCATTTAATCCTGGAGTTTTTTGTTGCAAACCTGACGGAATGGAAACGACAGAATATAACTA
ACCAACTGGAAAAATGGATGAAACTCAATGTAGAAGAGGGACTGTATAGCAGAACCTGGCT
GGTAGCATCACAAACACCTCCTCTGCTTATCGTATTTTATCAACAGCACTCTACCATCGATCC
TATGTGGAATGTCCGCCACCTTGGTTCCAGTGCTGGAAAACGATATTCACCTCAGTTTGTAA
AGGCTGCCAAGTTACTCCATTGGAATGGACATTTGAAGCCATGGGGAAGGACTGCTTCATAT
ACTGATGTTTGGGAAAAATGGTATATTCCAGACCCAACAGGCAAATTCAACCTAATCCGAAG
ATATACCGAGATCTCAAACATAAAGTGAACAG AATTTGAACTGTAAGCAAGCATTTCTCAG
GAAGTCCTGGAAGATAGCATGCATGGGAAGTAACAGTTGCTAGGCTTCAATGCCTATCGGTA
GCAAGCCATGGAAAAAGATGTGTCAGCTAGGTAAAGATGACAACTGCCCTGTCTGGCAGTC
AGCTTCCCAGACAGACTATAGACTATAAATATGTCTCCATCTGCCTTACCAAGTGTTTTCTT
ACTACAATGCTGAATGACTGGAAAGAAGAACTGATATGGCTAGTTCAGCTAGCTGGTACAGA
TAATTCAAAACTGCTGTTGGTTTTTAATTTTGTAACCTGTGGCCTGATCTGTAAATAAACTT
ACATTTTTC

FIGURE 105

MSFRKVNIIILVLAVALFLLVLHHNFLSLSSLLRNEVTD SGIVGPQPIDFVPNALRHAVDGR
QEEIPVVIAASEDR LGGAIAAINS IQHNTRS NVIFYIVTLNNTADHLRSWLNSDSLKSIRYK
IVNFDPKLLEGKV KEDPDQGESMKPLTFARFYLPILVPSAKKAIYMDDDVIVQGDILALYNT
ALKPGHAAAFSEDCDSASTKV VIRGAGNQYNYIGYLDYKKERIRKLSMKASTCSFNPGVFVA
NLTEWK RQNITNQLEKWMKLNVEEGLYSRTL AGSITTPPLLIVFYQQHSTIDPMWNVRLGS
SAGKRYSPQFVKAAKLLHWNGHLKPWGRTASYTDVWEKWYIPDPTGKFNLIRRYTEISNIK

0994164-44604

FIGURE 106

TGGTTTTTGCCCCATAAATTCCTCAGCTTGAGCAGTTTGTTAAGGAATGAGGTTACAGATT
CAGGAATTNTAGGNCCTCAACCTNTAGANTTTGTCCCAAATGTTCTCCGACATGCAGTAGAT
GGGAGACAAGAGGAGATTTCCTGTGGTCATCGCTGCATNTGAAGACAGGCTTGGGGGGGCCAT
TGCAGCTATAAACAGCATTTCAGCACAACTCGNTCCAATGTGATTTTCTACATTGTTACTC
TCAACAATACAGCAGACCATNTCCGGTCCTGGNTCAACAGTGATTCCCTGAAAAGCATCAGA
TACAAAATTGTCAATTTTGACCCTAACTTTTGGAAGGAAAAGTAAAGGAGGATCCTGACCA
GGGGGAATCCATGAAACCTTTAACCTTTGCAAGGTTCTACTTGCCAATTCTGGTTCCCAGCG
CAAAGAAGGCCATATACATGGATGATGATGTAATTGTGCAAGGTGATATTCTTGCCCTTTAC
AATACAGCACTGAAGCCAGGACATGCAGCTGCATTTTCAGAAGATTGTGATTCAGCCTCTAC
TAAAGTTGTCATCCGTGGAGCAGGAAA

FIGURE 107

CGACGCTCTAGCGGTTACCGCTGCGGGCTGGCTGGGCGTAGTGGGGCTGCGCGGCTGCCACG
GAGCTAGAGGGCAAGTGTGCTCGGCCCAGCGTGCAGGGAACGCGGGCGGCCAGACAACGGGC
TGGGCTCCGGGGCCTGCGGCGCGGGCGCTGAGCTGGCAGGGCGGGTCGGGGCGCGGGCTGCA
TCCGCATCTCCTCCATCGCCTGCAGTAAGGGCGGCCGCGGCGAGCCTTTGAGGGGAACGACT
TGTCGGAGCCCTAACCAGGGGTGTCTCTGAGCCTGGTGGGATCCCCGGAGCGTCACATCACT
TTCCGATCACTTCAAAGTGGTTAAAACTAATATTTATATGACAGAAGAAAAAGATGTCATT
CCGTAAAGTAAACATCATCATCTTGGTCTGGGCTGTTGCTCTCTTCTTACTGGTTTTGCAC
CATAACTTCCTCAGCTTGAGGCAGTTTGTTAAGGAATGAGGTTACAGATTGAGGAATTGTAG
GGCCTCAACCTATAGGACTTTGTCCCAAATGCTCTCCGACATGCAGTAGATGGGAGACAAGA
GGAGATTCCTGTGGTCATCGCTGCATCTGAAGACAGGCTTGGGGGGGCCATTGCAGCTATAA
ACAGCATTCAGCACAACTCGCTCCAATGTGATTTTCTACATTGTTACTCTCAACAATACA
GCAGACCATCTCCGGTCCTGGGCTCAACAGTGATTCCTGAAAAGCATCAGATACAAAATTG
TCAATTTTGACCCTAACTTTTGGAAGGAAAAGTAAAGGAGGATCCTGACCAGGGGGAATCC
ATGAAACCTTTAACCTTTGCAAGGTTCTACTTGCCAATTCTGGGTTCCCAGCGCAAAGAAGG
CCATATACATGGATGATGATGTAATTGTGCAAGGTGATATTCTTGCCCTTTACAATACAGCA
CTGAAGCCAGGACATGCAGCTGCATTTTCAGAAGATTGTGATTCAGCCTCTACTAAAGTTGT
CATCCGTGGAGCAGGAAACCAGTACAATTACATTGGCTATCTTGACTATAAAAAGGAAAGAA
TTCGTAAGCTTTCCATGAAAGCCAGCACTTGCTCATTTAATCCTGGAGTTTTTGTGCAAAC
CTGACGGAATGGAAACGACAGAATATACTAACCAACTGGAAAAATGGATGAACTCAATGT
AGAAGAGGGACTGTATAGCAGAACCCTGGCTGGTAGCATCACAAACACCTCCTCTGCTTATCG
TATTTTATCAACAGCACTCTACCATCGATCCTATGTGGAATGTCCGCCACCTTGGTTCCAGT
GCTGGAAAACGATATTCACCTCAGTTTGTAAAGGCTGCCAAGTTACTCCATTGGAATGGACA
TTTGAAGCCATGGGGAAGGACTGCTTCATATACTGATGTTTGGGGAAAAATGGTATATTCCA
GACCCAACAGGCAAATTCAACCTAATCCGAAGATATACCGAGATCTCAAACATAAAGTGAAA
CAGAATTTGAACTGTAAGCAAGCATTTCTCAGGAAGTCCTGGAAGATAGCATGCGTGGGAAG
TAACAGTTGCTAGGCTTCAATGCCTATCGGTAGCAAGCCATGGAAAAAGATGTGTCAGCTAG
GTAAAGATGACAACTGCCCTGTCTGGCAGTCAGCTTCCCAGACAGACTATAGACTATAAAT
ATGTCTCCATCTGCCTTACCAAGTGTTTTCTTACTACAATGCTGAATGACTGGAAAGAAGAA
CTGATATGGCTAGTTCAGCTAGCTGGTACAGATAATTCAAACTGCTGTTGGTTTTAATTTT
GTAACCTGTGGCCTGATCTGTAAATAAACTTACATTTTTCAATAGGTAAAAA

CTGCAGGTAGACATCTCCACTGCCAGGAATCACTGAGCGTGCAGACAGCACAGCCTCCTCT
GAAGGCCGGCCATAACCAGAGTCTTGCCTCGGCATGGGCCTCACCATTGAGGCAGCTCCACTG
TCTGTGCTGGTCTGAGGGTGCTGCCTGTC**ATG**GGGGCAGCCATCTCCAGGGGGCCCTCATC
GCCATCGTCTGCAACGGTCTCGTGGGCTTCTTGCTGCTGCTGCTCTGGGTCTATCCTCTGCTG
GGCCTGCCATTCTCGTCTGCCGACGTTGACTCTCTCTCTGAATCCAGTCCCAACTCCAGCCC
TGGCCCCTGTCCTGAGAAGGCCCCACCACCCCAGAAGCCCAGCCATGAAGGCAGCTACCTGC
TGCAGCCCTGAAGGCCCTGGCCTAGCCTGGAGCCCAGGACCT**TAA**GTCCACCTCACCTAGAG
CCTGGAATTAGGATCCCAGAGTTCAGCCAGCCTGGGGTCCAGAACTCAAGAGTCCGCCTGCT
TGGAGCTGGACCCAGCGGCCCAGAGTCTAGCCAGCTTGGCTCCAATAGGAGCTCAGTGGCCC
TAAGGAGATGGGCCTGGGGTGGGGGCTTATGAGTTGGTGCTAGAGCCAGGGCCATCTGGACT
ATGCTCCATCCCAAGGGCCAAGGGTCAGGGGCCGGGTCCACTCTTTCCCTAGGCTGAGCACC
TCTAGGCCCTCTAGGTTGGGGAAGCAAACCTGGAACCCATGGCAATAATAGGAGGGTGTCCAG
GCTGGGGCCCCTCCCCTGGTCCTCCCAGTGTTTGCTGGATAATAAATGGAACCTATGGCTCTAA
AAAAAAAAAAAAAAAAAAAA

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FIGURE 109

MGAAISQGALIAIVCNGLVGFLLLLLWVILCWACHSRLPTLTLSLNPVPTPALAPVLRRPHH
PRSPAMKAATCCSPEGPWPSLEPRT

0944134660

FIGURE 110

GTTGAATTCCTTCAACTATACCCACAGTCCAAAAGCAGACTCACTGTGTCCCAGGCTACCA
 GTTCCTCCAAGCAAGTCATTTCCCTTATTTAACCGATGTGTCCCTCAAACACCTGAGTGCTA
 CTCCCTATTTGCATCTGTTTTGATAAATGATGTTGACACCCTCCACCGAATTCTAAGTGGAA
 TC**ATG**TCGGGAAGAGATACAATCCTTGGCCTGTGTATCCTCGCATTAGCCTTGTCTTTGGCC
 ATGATGTTTACCTTCAGATTCATCACCACCCTTCTGGTTCACATTTTCATTTTCATTGGTTAT
 TTTGGGATTGTTGTTTGTCTGCGGTGTTTTATGGTGGCTGTATTATGACTATACCAACGACC
 TCAGCATAGAATTGGACACAGAAAGGGAAAATATGAAGTGCCTGCTGGGGTTTGCTATCGTA
 TCCACAGGCATCACGGCAGTGCTGCTCGTCTTGATT'TTTGTTCTCAGAAAGAGAATAAAATT
 GACAGTTGAGCT'TTTCCAAATCACAAATAAAGCCATCAGCAGTGCTCCCTTCCTGCTGTTCC
 AGCCACTGTGGACATTTGCCATCCTCATTTTCTTCTGGGTCTCTGGGTGGCTGTGCTGCTG
 AGCCTGGGAAGTGCAGGAGCTGCCAGGTTATGGAAGGCGGCCAAGTGGAATATAAGCCCCCT
 TTCGGGCATTTCGGTACATGTGGTCGTACCATT'TAATTGGCCTCATCTGGACTAGTGAATTCA
 TCCTTGCGTGCCAGCAAATGACTATAGCTGGGGCAGTGGTTACTTGTTATTTCAACAGAAGT
 AAAAATGATCCTCCTGATCATCCCATCCTTTCTGCTCTCTCTCCATTCTCTTCTTCTACCATCA
 AGGAACCGTTGTGAAAGGGTCATTTTAAATCTCTGTGGTGAGGATTCCGAGAATCATTGTCA
 TGTACATGCAAAACGCACTGAAAGAACAGCAGCATGGTGCATTGTCCAGGTACCTGTTCCGA
 TGCTGCTACTGCTGTTTCTGGTGTCTTGACAAATACCTGCTCCATCTCAACCAGAATGCATA
 TACTACAACCTGCTATTAATGGGACAGATTTCTGTACATCAGCAAAAGATGCATTCAAAATCT
 TGTCCAAGAACTCAAGTCACTTTACATCTATTAAGTCTTTGGAGACTTCATAATTTTCTA
 GGAAAGGTGTTAGTGGTGTGTTTCACTGTTTTTGGAGGACTCATGGCTTTTAACTACAATCG
 GGCATTCCAGGTGTGGGCAGTCCCTCTGTTATTGGTAGCTTTTTTTGCCTACTTAGTAGCCC
 ATAGTTTTTTTATCTGTGTTTGAAACTGTGCTGGATGCAC'TTTCCTGTGTTTTGCTGTTGAT
 CTGGAAACAAATGATGGATCGTCAGAAAAGCCCTACTTTATGGATCAAGAATTTCTGAGTTT
 CGTAAAAAGGAGCAACAAATTAAACAATGCAAGGGCACAGCAGGACAAGCACTCATTAAGGA
 ATGAGGAGGGAACAGAACTCCAGGCCATTGTGAGAT**TAG**ATAACCATTTAGGTATCTGTACCT
 GGAAAACATTTCTTCTAAGAGCCATTTACAGAATAGAAGATGAGACCACTAGAGAAAAGTT
 AGTGAATTTTTTTTTTAAAAGACCTAATAAACCTATTCTTCCTCAAAA

MSGRDTILGLCILALALSLAMMFTFRFITTLVHIFISLVILGLLFVCGVLWWLYDYDYNL
SIELDTERENMKCVLGFAIVSTGITAVLLVLI FVLRKRIKLTVELFQITNKAISSAPFLLFQ
PLWTFAILIFFWVLWVAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYMWSYHLIGLIWTSEFI
LACQQMTIAGAVVTCYFNRSKNDPPDHPILSSLSILFFYHQGTVVKGSFLISVVRIPIIVM
YMQNALKEQQHGALSRYLFRCCYCCFWCLDKYLLHLNQAYTTTAINGTDFCTSAKDAFKIL
SKNSSHFTSINCFGDFIIFLGKVLVVCFTVFGGLMAFNYNRAFQVWAVPLLLVAFFAYLVAH
SFLSVFETVLDALFLCFAVDLETNDGSSEKPYFMDQEFLSFVKRSNKLNNARAQQDKHSLRN
EEGTELQAIVR

MRTVVLTMKASVIEMFLVLLVTGVHSNKETAKKIKRPFKFTVPQINCDVKAGKIIDPEFIVKC
PAGCQDPKYHVYGTDVYASYSSVCGAAVHSGVLDNSGGKILVRKVAGQSGYKGSYSNGVQSL
SLPRWRESFIVLESKPKKGVITYPSALTYSSSKSPAAQAGETTKAYQRPPIPGTTAQPVITLMQ
LLAVTVAVATPTTLPRPSPSAASTTSIPRPQSVGHRSEQEMDLWSTATYTSQNRPRADPGIQ
RQDPSGAAFQKPVGADVSLGLVPKEELSTQSLEPVSLGDPNCKIDLSFLIDGSTSIGKRRFR
IQKQLLADVAQALDIGPAGPLMGVVQYGDNPATHFNLKTHTNRSRDLKTAIEKITQRGGLSNV
GRAISFVTKNFFSKANGNRSGAPNVVVVMVDGWPTDKVEEASRLARESGINIFFITIEGAAE
NEKQYVVEPNFANKAVCRTNGFYSLHVQSWFGLHKTLOPLVKRVCDTDRLACSKTCLNSADI
GFVIDGSSSVGTGNFRTVLQFVTNLTKEFEISDTDTRIGAVQYTYEQRLEFGFDKYSSKPD
LNAIKRVGYWSGGTSTGAAINFALEQLFKKSKPNKRKLMILITDGRSYDDVRI PAMAAHLKG
VITYAIGVAWAAQEELEVIATHPARDHSFFVDEFDNLHQYVPRI IQNICTEFNSQPRN

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FIGURE 115

MPFRLLIPLGLLCALLPQHHGAPGPDGSAPDPAHYSFSLTLIDALDTLLILGNVSEFQRVVE
VLQDSVDFDIDVNASVFETNIRVVGGLLSAHLLSKKAGVEVEAGWPCSGPLLMAEEAARKL
LPAFQTPTGMPYGTVNLLHGVNPGETPVTCTAGIGTFIVEFATLSSLTGDPVFEDVARVALM
RLWESRSDIGLVGNHIDVLTGKWVAQDAGIGAGVDSYFEYLVKGAILLQDKKLMAMFLEYNK
AIRNYTRFDDWYLVWQMYKGTVSMPVFQSLEAYWPGLOSLIGDIDNAMRTFLNYYTVWKQFG
GLPEFYNIPOGYTVEKREGYPLRPELIESAMYLYRATGDPTLLELGRDAVESIEKISKVECG
FATIKDLRDHKLDNRMESFFLAETVKYLYLLFDPTNFIHNNGSTFDAVITPYGECILGAGGY
IFNTEAHPIDLAALHCCQRLKEEQWEVEDLMREFYSLKRSRSKFQKNTVSSGPWEPPARPGT
LFSPENHDQARERKPAKQKVPLLSCPSQPFTSKLALLGQVFLDSS

“F.T.F.” T.F.T.F.F.

FIGURE 116

AAAGTTACATTTTCTCTGGAACCTCTCCTAGGCCACTCCCTGCTGATGCAACATCTGGGTTTG
 GGCAGAAAGGAGGGTGCTTCGGAGCCCCGCCCTTTCTGAGCTTCCTGGGCCGGCTCTAGAACA
 ATTCAGGCTTCGCTGCGACTCAGACCTCAGCTCCAACATATGCATTCTGAAGAAAGATGGCT
 GAGATGGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGGTCAAACCTGAGTCTACCA
AATGCAGACTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCTTTTCATGTGGTTTTTCT
 ACGCATTGATTCCATGTTTGCTCACAGATGAAGTGCCATTCTGCCTGCCCCTCAGAACCTC
 TCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCCAGTGATCGCGCCTGGAGA
 AACAGTGTAATCTGTGCGAATACCAGGGGGAGTACGAGAGCCTGTACACGAGCCACATCT
 GGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCTGAGTGTGATGTCACTGATGACATC
 ACGGCCACTGTGCCATACAACCTTCGTGTCAGGGCCACATTGGGCTCACAGACCTCAGCCTG
 GAGCATCCTGAAGCATCCCTTTAATAGAACTCAACCATCCTTACCCGACCTGGGATGGAGA
 TCACCAAAGATGGCTTCCACCTGGTTATTGAGCTGGAGGACCTGGGGCCCCAGTTTGAGTTC
 CTTGTGGCCTACTGGAGGAGGGAGCCTGGTGCCGAGGAACATGTCAAAATGGTGAGGAGTGG
 GGGTATTCCAGTGACCTAGAAACCATGGAGCCAGGGGCTGCATACTGTGTGAAGGCCCAGA
 CATTCTGTGAAGGCCATTGGGAGGTACAGCGCCTTCAGCCAGACAGAATGTGTGGAGGTGCAA
 GGAGAGGCCATTCCCCTGGTACTGGCCCTGTTTGCCTTTGTTGGCTTCATGCTGATCCTTGT
 GGTCGTGCCACTGTTCTGTGAAAATGGGCCGGCTGCTCCAGTACTCCTGTTGCCCCGTGG
 TGGTCCTCCCAGACACCTTGAAAATAACCAATTCACCCCAGAAGTTAATCAGCTGCAGAAGG
 GAGGAGGTGGATGCCTGTGCCACGGCTGTGATGTCTCCTGAGGAACTCCTCAGGGCCTGGAT
 CTCATAGTGTGCGGAAGGGCCCAGGTGAAGCCGAGAACCTGGTCTGCATGACATGGAAACC
 ATGAGGGGACAAGTTGTGTTTCTGTTTTCCGCCACGGACAAGGGATGAGAGAAGTAGGAAGA
 GCCTGTTGTCTACAAGTCTAGAAGCAACCATCAGAGGCAGGGTGGTTTGTCTAACAGAACAC
 TGAAGTGAAGCTTAGGGGATGTGACCTCTAGACTGGGGGCTGCCACTTGCTGGCTGAGCAACC
 CTGGGAAAAGTGACTTCATCCCTTCGGTCCTAAGTTTTCTCATCTGTAATGGGGGAATTACC
 TACACACCTGCTAAACACACACACACAGAGTCTCTCTCTATATATACACACGTACACATAAA
 TACACCCAGCACTTGCAAGGCTAGAGGGAACTGGTGACACTCTACAGTCTGACTGATTAG
 TGTTTCTGGAGAGCAGGACATAAATGTATGATGAGAATGATCAAGGACTCTACACACTGGGT
 GGCTTGGAGAGCCCACTTTCCAGAAATAATCCTTGAGAGAAAAGGAATCATGGGAGCAATGG
 TGTGAGTTCACTTCAAGCCCAATGCCGGTGAGAGGGGAATGGCTTAGCGAGCTCTACAGT
 AGGTGACCTGGAGGAAGGTCACAGCCACACTGAAAATGGGATGTGCATGAACACGGAGGATC
 CATGAACTACTGTAAAGTGTGACAGTGTGTGCACACTGCAGACAGCAGGTGAAATGTATGT
 GTGCAATGCGACGAGAATGCAGAAGTCAGTAACATGTGCATGTTTGTGTGCTCCTTTTTTC
 TGTTGGTAAAGTACAGAATTACAGCAAATAAAAAGGGCCACCCTGGCCAAAAGCGGTAAAAAA
 AAAAAAAAAA

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FIGURE 117

MQTFTMVLEEIWTSLFMWFFYALIPCLLTDEVAILPAPQNLSVLSTNMKHLMLWSPVIAPGE
TVYYSVEYQGEYESLYTSHIWIPSSWCSLTEGPECDVTDDITATVPYNLRVRATLGSQTS
SILKHPFNRNSTILTRPGMEITKDGFLVIELEDLGPQFEFLVAYWRREPGAEEHVKMVRSG
GIPVHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTECVEVQGEAIPVLALFAFVGFMILILV
VVPLFVWKMGRLLQYSCCPVVVLPDTLKITNSPQKLISCRREEVDACATAVMSPEELLRAWIS

Important features:

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 230-255

N-glycosylation sites.

amino acids 40-43 and 134-137

Tissue factor proteins homology.

amino acids 92-119

Integrins alpha chain protein homology.

amino acids 232-262

TC9TTF" T8TF65D

FIGURE 118

TCCTGCTGATGCACATCTGGGTTTGGCAAAGGAGGTTGCTTCGAGCCGCCCTTTCTAGCTT
CCTGGCCGGCTCTAGAACAATTCAGGCTTCGCTGCGACTAGACCTCAGCTCCAACATATGCA
TTCTGAAGAAAGATGGCTGAGATGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGG
TCAAACCTGAGTCTACCAAATGCAGACTTTTACAATGGTTCTAGAAGAAATCTGGACAAGTCT
TTTCATGTGGTTTTTCTACGCATTGATTCCATGTTTGCTCACAGATGAAGTGGCCATTCTGC
CTGCCCCCTCAGAACCTCTCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCCA
GTGATCGCGCCTGGAGAAACAGTGTACTATTCTGTCTGAATACCAGGGGGAGTACGAGAGCCT
GTACACGAGCCACATCTGGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCCTGAGTGTG
ATGTCACTGATGACATCACGGCCACTGTGCCATACAACCTTTGTGTCAGGGCCACATTGGGC
TCACAGACCTCAGCCTGGAGCATCCTGAAGCATCCCTTTAATAGAAACTCAACCATCCTTAC
CCGACCTGGGATGGAGATCACCAAAGATGGCTTNCACCTGGTTATTGAGCTGGAGGACCTGG
GGCCCCAGTTTGAGTTCCTTGTGGCCTANTGGAGGAGGGGCGAACCCCTTGCGGCGCAAGGG
GTTNGCGAACCCCTTGCGGCCGCTGGGGTATCTCTCGAGAAAAGAGAGGCCCAATATGACCCAC
ATACTCAATATGGACGAANTGCTATTGTCCACCTGTTTGAGTGGCGCTGGGGTTGAT

FIGURE 119

CGGACGCGTGGGCCGCCACCTCCGGAACAAGCC**ATG**GTGGCGGCGACGGTGGCAGCGGCGTG
GCTGCTCCTGTGGGCTGCGGCCTGCGCGCAGCAGGAGCAGGACTTCTACGACTTCAAGGCGG
TCAACATCCGGGGCAAACCTGGTGTGCTGGAGAAGTACCGCGGATCGGTGTCCCTGGTGGTG
AATGTGGCCAGCGAGTGC GGCTTACAGACCAGCACTACCGAGCCCTGCAGCAGCTGCAGCG
AGACCTGGGGCCCCACCACTTTAACGTGCTCGCCTTCCCCTGCAACCAGTTTGGCCAACAGG
AGCCTGACAGCAACAAGGAGATTGAGAGCTTTGCCCCGCCGACCTACAGTGTCTCATTTCCC
ATGTTTAGCAAGATTGCAGTCACCGGTACTGGTGCCCATCCTGCCTTCAAGTACCTGGCCCA
GACTTCTGGGAAGGAGCCCACCTGGAACCTCTGGAAGTACCTAGTAGCCCCAGATGGAAAGG
TGGTAGGGGCTTGGGACCCAACTGTGTGAGTGGAGGAGGTCAGACCCCAGATCACAGCGCTC
GTGAGGAAGCTCATCCTACTGAAGCGAGAAGACTT**TAA**ACCACCGCGTCTCCTCCTCCACCA
CCTCATCCCGCCCACCTGTGTGGGGCTGACCAATGCAAACCTCAAATGGTGCTTCAAAGGGAG
AGACCCACTGACTCTCCTTCCTTTACTCTTATGCCATTGGTCCCATCATTCTTGTGGGGGAA
AAATTCTAGTATTTTGATTATTTGAATCTTACAGCAACAAATAGGAACCTCCTGGCCAATGAG
AGCTCTTGACCAGTGAATCACCAGCCGATACGAACGTCTTGCCAACAAAAATGTGTGGCAAA
TAGAAGTATATCAAGCAATAATCTCCCACCCAAGGCTTCTGTAAACTGGGACCAATGATTAC
CTCATAGGGCTGTTGTGAGGATTAGGATGAAATACCTGTGAAAGTGCCTAGGCAGTGCCAGC
CAAATAGGAGGCATTCAATGAACATTTTTTGCATATAAACCAAAAAATAACTTGTTATCAAT
AAAAACTTGCATCCAACATGAATTTCCAGCCGATGATAATCCAGGCCAAAGGTTTAGTTGTT
GTTATTTCTCTGTATTATTTTCTTCATTACAAAAGAAATGCAAGTTCATTGTAAACAATCCA
ACAATACCTCACGATATAAAATAAAAATGAAAGTATCCTCCTCAAAA

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FIGURE 120

MVAATVAAAWLLLWAAACAQQEQDFYDFKAVNIRGKLVSLEKYRGSVSLVVNVASECGFTDQ
HYRALQQLQRDLGPHHFNVLAFFPCNQFGQQEPDSNKEIESFARRTYSVSFPMFSKIAVTGTG
AHPAFKYLAQTSGKEPTWNFWKYLVPDGVVGAWDPTVSVEEVRPQITALVRKLILLKREDL

protein structure

CGGACGCGTGGGCGGGCGGGACGCGAGGCCAAGCGAGGCC**ATGG**CTGTCTACGTCGGGATGCTGCGCCTGGGGAGGCTGTGCGCCGGGAGCTCGGGGGTGTCTGGGGGCCCGGGCCGCCCTCTCTCGGAGTTGGCAGGAAGCCAGGTTGCAGGGTGTCCGCTTCTCTCAGTTCCAGAGAGGTGGATCGCATGGTCTCCACGCCCATCGGAGGCCTCAGCTACGTTTCAGGGGTGCACCAAAAAGCATCTTACAGCAAGACTGTGGGCCAGTGCCTGGAGACCACAGCACAGAGGGTCCCAGAACGAGAGGCCTTGGTTCGTCTCTCCATGAAGACGTCAGGTTGACCTTTGCCCAACTCAAGGAGGAGGTGGACAAAGCTGCTTCTGGCCTCCTGAGCATTGGCCTCTGCAAAGGTGACCGGCTGGGCATGTGGGGACCTAACTCCTATGCATGGGTGCTCATGCAGTTGGCCACCGCCCAGGCGGGGCATCATTTCTGGTGCTGTGAACCCAGCCTACCAGGCTATGGAAGTGGAGTATGTCTCAAGAAGGTGGGCTGCAAGGCCCTTGTGTTCCCAAGCAATTCAAGACCCAGCAATACTACAACGTCCTGAAGCAGATCTGTCCAGAAGTGGAGAATGCCAGCCAGGGGCTTGAAGAGTCAGAGGCTCCCAGATCTGACCACAGTCATCTCGGTGGATGCCCTTTGCCGGGGACCCTGCTCCTGGATGAAGTGGTGGCGGC TGGCAGCACACGGCAGCATCTGGACCAGCTCCAATACAACCAGCAGTTCTGTCTTGCCATGACCCCATCAACATCCAGTTCACCTCGGGGACAACAGGCAGCCCCAAGGGGGGCCACCCTCTCCACTACAACATTGTCAACAACTCCAACATTTTAGGAGAGCGCTGAAACTGCATGAGAAGACACCAGAGCAGTTGCGGATGATCCTGCCCCAACCCCTGTACCATTGCCTGGGTTCGTGGCAGGCACAATGATGTGTCTGATGTACGGTGCCACCCTCATCCTGGCCTCTCCCATCTTCAATGGCAAGAAGGCACTGGAGGCCATCAGCAGAGAGAGAGGGCACCTTCTGTATGGTACCCCCACGATGTTTCGTGGACATTCTGAACCAGCCAGACTTCTCCAGTTATGACATCTCGACCATGTGTGGAGGTGTCAATTGCTGGGTCCCCTGCACCTCCAGAGTTGATCCGAGCCATCATCAACAAGATAAATATGAAGGACCTGGTGGTTGCTTATGGAACCACAGAGAACAGTCCCGTGACATTCGCGCACTTCCCTGAGGACACTGTGGAGCAGAAGGCAGAAAGCGTGGGCAGAATTATGCCTCACACGGAGGCCGGATCATGAACATGGAGGCAGGGACGCTGGCAAAGCTGAACACGCCCGGGGAGCTGTGCATCCGAGGGTACTGCGTCATGCTGGGCTACTGGGGTGAGCCTCAGAAGACAGAGGAAGCAGTGGATCAGGACAAGTGGTATTGGACAGGAGATGTGCCACAATGAATGAGCAGGGCTTCTGCAAGATCGTGGGCCGCTCTAAGGATATGATCATCCGGGGTGGTGAGAACATCTACCCCGCAGAGCTCGAGGACTTCTTTCACACACACCCGAAGGTGCAGGAAGTGCAGGTGGTGGGAGTGAAGGACGATCGGATGGGGGAAGAGATTTGTGCCTGCATTCGGCTGAAGGACGGGGAGGAGACCACGGTGGAGGAGATAAAAGCTTTCTGCAAAGGGAAGATCTCTCACTTCAAGATTCCGAAGTACATCGTGTGTTGTACAAACTACCCCTCACCATTTCAGGAAAGATCCAGAAATTCAAACCTTCGAGAGCAGATGGAACGACATCTAAATCTG**TGA**ATAAAGCAGCAGGCCTGTCCTGGCCGGTTGGCTTGACTCTCTCCTGTCAGAATGCAACCTGGCTTTATGCACCTAGATGTCCCCAGCACCCAGTTC TGAGCCAGGCACATCAAATGTCAAGGAATTGACTGAACGAACTAAGAGCTCCTGGATGGGTCCGGAACTCGCCTGGGCACAAGGTGCCAAAAGGCAGGCAGCCTGCCAGGCCCTCCCTCCTGTCCATCCCCCACATTCCCCTGTCTGTCTTGTGATTGGCATAAAGAGCTTCTGTTTTCTTTGAAAAAAAAAAAAAAAAA

FIGURE 122

MAVYVGMLRLGRLCAGSSGVLGARAALSRSWQEARLQGVRFLSSREVD RMVSTPIGGLSYVQ
GCTKKHLNSKTVGQCLETTAQRVPEREALVVLHEDVRLTFAQLKEEVDKAASGLLSIGLCKG
DRLGMWGPNSYAWVLMQLATAQAGIILVSVNPAYQAMELEYVLKKVGCKALVFPKQFKTQQY
YNVLKQICPEVENAQPGALKSQRLPDLTTVISVDAPLPGTLLLDEVVAAGSTRQHLDQLQYN
QQFLSCHDPINIQFTSGTTGSPKGATLSHYNIVNNSNILGERLKLHEKTPEQLRMILPNPLY
HCLGSVAGTMMCLMYGATLILASPIFNGKKALEAISRERGTFLYGTPTMFVDILNQPDFSSY
DISTMCGGVIAGSPAPPELIRAIINKINMKDLVVAYGTTENSPVTFAHFPEDTVEQKAESVG
RIMPHTEARIMNMEAGTLAKLNTPGELCIRGYCVMLGYWGEPQKTEEAVDQDKWYWTGDVAT
MNEQGFCIVGRSKDMIIRGGENIYPAELEDFHHPKVQEVQVVGVKDDRMGEEICACIRL
KDGEETTVEEIKAFCKGKISHFKIPKYIVFVTNYPLTISGKIQKFKLREQMERHLNL

Signal Peptide:

amino acids 1-22

Transmembrane Domains:

amino acids 140-161, 213-229, 312-334

Putative AMP-binding Domain Signature:

amino acids 260-271

N-myristoylation Sites:

amino acids 19-24, 22-27, 120-125, 203-208, 268-273, 272-277,
314-319, 318-323, 379-384, 380-385, 409-413

N-glycosylation Site:

amino acids 282-285

FIGURE 123

CAACTCCAACATTTTAGGAGAGCGCCTGAAACTGCATGAGAAGACACCAGAGCAGTTGCGGA
TGATCCTGCCCAACCCCCTGTACCATTCCTGGGTTCGTGGCAGGCACAATGATGTGTCTG
ATGTACGGTGCCACCCTCATCCTGGCCTCTCCCATCTTCAATGGCAAGAAGGCACTGGAGGC
CATCAGCAGAGAGAGAGGCACCTTCCTGTATGGTACCCCCACGATGTTTCGTGGACATTCTGA
ACCAGCCAGACTTCTCCAGTTATGACATCTCGACCATGTGTGGAGGTGTCATTGCTGGGTCC
CCTGCACCTCCAGAGTTGATCCGAGCCATCATCAACAAGATAAATATGAAGGACCTGGTGGT
TGCTTATGGAACCACAGAGAACAGTCCCGTGACATTCGCGCACTTCCCTGAGGACACTGTGG
AGCAGAAGGCAGAAAGCGTGGGCAGAATTATGCCTCACACGGAGGCGCGGATCATGAACATG
GAGGCAGGGACGCTGGCAAAGCTGAACACGCCCCGGGGAGCTGTGCATCCGAGGGTACTGCGT
CATGCTGGGCTACTGGGGTGAGCCTCAGAAGACAGAGGAAGCAGTGGATCAGGACAAGTGGT
ATTGGACAGGAGATGTCGCCAC

GAGCAGGACGGAGCCATGGACCCCGCCAGGAAAGCAGGTGCCCAGGCCATGATCTGGACTGC
AGGCTGGCTGCTGCTGCTGCTGCTTCGCGGAGGAGCGCAGGCCCTGGAGTGCTACAGCTGCG
TGCAGAAAGCAGATGACGGATGCTCCCCGAACAAGATGAAGACAGTGAAGTGCGCGCCGGGC
GTGGACGTCTGCACCGAGGCCGTGGGGGCGGTGGAGACCATCCACGGACAATTCTCGCTGGC
AGTGCGGGGTTCGCGTTTCGGGACTCCCCGGCAAGAATGACCGCGGCCTGGATCTTCACGGGC
TTCTGGCGTTCATCCAGCTGCAGCAATGCGCTCAGGATCGCTGCAACGCCAAGCTCAACCTC
ACCTCGCGGGCGCTCGACCCGGCAGGTAATGAGAGTGCATACCCGCCCAACGGCGTGGAGTG
CTACAGCTGTGTGGGCCTGAGCCGGGAGGCGTGCCAGGGTACATCGCCGCCGGTTCGTGAGCT
GCTACAACGCCAGCGATCATGTCTACAAGGGCTGCTTCGACGGCAACGTCACCTTGACGGCA
GCTAATGTGACTGTGTCTTGCCTGTCCGGGGCTGTGTCCAGGATGAATTCTGCACTCGGGA
TGGAGTAACAGGCCCAGGGTTCACGCTCAGTGGCTCCTGTTGCCAGGGGTCCCGCTGTAACCT
CTGACCTCCGCAACAAGACCTACTTCTCCCCTCGAATCCCACCCCTTGTCCGGCTGCCCCCT
CCAGAGCCACGACTGTGGCCTCAACCACATCTGTCACCACTTCTACCTCGGCCCCAGTGAG
ACCCACATCCACCACCAAACCCATGCCAGCGCCAACCAGTCAGACTCCGAGACAGGGAGTAG
AACACGAGGCCTCCCGGGATGAGGAGCCCAGGTTGACTGGAGGCGCCGCTGGCCACCAGGAC
CGCAGCAATTACAGGGCAGTATCCTGCAAAAGGGGGGCCCCAGCAGCCCCATAATAAAGGCTG
TGTGGCTCCACAGCTGGATTGGCAGCCCTTCTGTTGGCCGTGGCTGCTGGTGTCTACTGTT
GAGCTTCTCCACCTGGAAATTTCCCTCTCACCTACTTCTCTGGCCCTGGGTACCCCTCTTCT
CATCACTTCCTGTTCCCACTGGACTGGGCTGGCCCAGCCCCTGTTTTTCCAACATTCCC
CAGTATCCCCAGCTTCTGCTGCGCTGGTTTTCGGGCTTTGGGAAATAAAATACCGTTGTATAT
ATTCTGCCAGGGGTGTTCTAGCTTTTTGAGGACAGCTCCTGTATCCTTCTCATCCTTGTCTC
TCCGCTTGTCTCTTGTGATGTTAGGACAGAGTGAGAGAAGTCAGCTGTCACGGGGAAGGTG
AGAGAGAGGATGCTAAGCTTCCTACTCACTTTCTCCTAGCCAGCCTGGACTTTGGAGCGTGG
GGTGGGTGGGACAATGGCTCCCCACTCTAAGCACTGCCTCCCCTACTCCCCGCATCTTTGGG
GAATCGGTTCCCATATGTCTTCCTTACTAGACTGTGAGCTCCTCGAGGGGGGGGCCCGGTAC
CCAATTCGCCCTATAGTGAGTCGTA

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FIGURE 125

MDPARKAGAQAMIWTAGWLLLLLLRGGAQALECYSCVQKADDGCSPNKMKTVKCAPGVDVCT
EAVGAVETIHGQFSLAVRGCGSGLPGKNDRGLDLHGLLAFIQLQOCAQDRCNAKLNLTSRAL
DPAGNESAYPPNGVECYSCVGLSREACQGTSPPVVSCYNASDHVYKGCDFGNVTLTAANVTV
SLPVRGCVQDEFCTR DGVTGPGFTLSGSCCQGSRCNSDLRNKTYFSPRIPLVRLPPPEPTT
VASTTSVTTST SAPVRPTSTTKPMPAPTSQTPRQGEHEASRDEEPRLTGGAAGHQDRSNSG
QYPAKGGPQQPHNKGCVAPTAGLAALLLAVAAGVLL

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FIGURE 126

CGGGACTCGGCGGGTCTCTGGGAGTCTCGGAGGGGACCGCTGTGCAGACGCC**ATG**GAGT
TGGTGCTGGTCTTCCTCTGCAGCCTGCTGGCCCCCATGGTCCTGGCCAGTGCAGCTGAAAAG
GAGAAGGAAATGGACCCTTTTTCATTATGATTACCAGACCCTGAGGATTGGGGGACTGGTGT
CGCTGTGGTCCTCTTCTCGGTTGGGATCCTCCTTATCCTAAGTCGCAGGTGCAAGTGCAGTT
TCAATCAGAAGCCCCGGGCCCCAGGAGATGAGGAAGCCCAGGTGGAGAACCCTCATCACCGCC
AATGCAACAGAGCCCCAGAAGCAGAGAACTGAAGTGCAGCCATCAGGTGGAAGCCTCTGGAA
CCTGAGGCGGCTGCTTGAACCTTTGGATGCAAATGTCGATGCT**TAA**GAAAACCGGCCACTTC
AGCAACAGCCCTTTCCCCAGGAGAAGCCAAGAACTTGTGTGTCCCCCACCTATCCCTCTA
ACACCATTCTCCACCTGATGATGCAACTAACACTTGCCCTCCCCACTGCAGCCTGCGGTCT
GCCACCTCCCGTGATGTGTGTGTGTGTGTGTGTGTGTGTGTGACTGTGTGTGTTTGCTAACTGTG
GTCTTTGTGGCTACTTGTTTGTGGATGGTATTGTGTTTGTAGTGAAGTGTGGACTCGCTTT
CCCAGGCAGGGGCTGAGCCACATGGCCATCTGCTCCTCCCTGCCCCCGTGGCCCTCCATCAC
CTTCTGCTCCTAGGAGGCTGCTTGTGCCCCGAGACCAGCCCCCTCCCCTGATTTAGGGATGC
GTAGGGTAAGAGCACGGGCAGTGGTCTTCAGTCGTCTTGGGACCTGGGAAGGTTTGCAGCAC
TTTGTTCATCATCTTCATGGACTCCTTTCACTCCTTTAACAAAAACCTTGCTTCCTTATCCC
ACCTGATCCCAGTCTGAAGGTCTCTTAGCAACTGGAGATACAAAGCAAGGAGCTGGTGAGCC
CAGCGTTGACGTCAGGCAGGCTATGCCCTTCCGTGGTTAATTTCTTCCCAGGGGCTTCCACG
AGGAGTCCCCATCTGCCCCGCCCTTCACAGAGCGCCGGGGATTCCAGGCCCAGGGCTTCT
ACTCTGCCCCCTGGGGAATGTGTCCCCTGCATATCTTCTCAGCAATAACTCCATGGGCTCTGG
GACCCCTACCCCTTCCAACCTTCCCTGCTTCTGAGACTTCAATCTACAGCCCAGCTCATCCAG
ATGCAGACTACAGTCCCTGCAATTGGGTCTCTGGCAGGCAATAGTTGAAGGACTCCTGTTCC
GTTGGGGCCAGCACACCGGGATGGATGGAGGGAGAGCAGAGGCCTTTGCTTCTCTGCCTACG
TCCCCCTTAGATGGGCAGCAGAGGCAACTCCCGCATCCTTTGCTCTGCCTGTTCGGTGGTCAGA
GCGGTGAGCGAGGTGGGTTGGAGACTCAGCAGGCTCCGTGCAGCCCTTGGGAACAGTGAGAG
GTTGAAGGTCATAACGAGAGTGGGAACCAACCCAGATCCCGCCCCCTCCTGTCCTCTGTGTT
CCCGCGGAAACCAACCAACCGTGCGCTGTGACCCATTGCTGTTCTCTGTATCGTGATCTAT
CCTCAACAACAACAGAAAAAAGGAATAAAATATCCTTTGTTTCCT

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FIGURE 127

MELVLVFLCSLLAPMVLASAAEKEKEMDPFHYDYQTLRIGGLVFAVVLFSVGILLILSRRCK
CSFNQKPRAPGDDEEAQVENLITANATEPQKQRTVEVQPSGGSLWNLRRLLEPLDANVDA

009461 44604
T09461 44604

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FIGURE 129

MKIPVLPVAVLLSLLVLHSAQGATLGGPEEESTIENYASRPEAFNTPFLNIDKLRSFAKDE
FLNWHALFESIKRKLPFLNWDAFPCLKGLRSATPDAQ

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FIGURE 130

CAGTTCTGAAATCAATGGAGTTAATTTAGGGAATACAAACCAGCC**ATG**GGGGTGGAGATTGC
CTTTGCCTCAGTGATTCTCACCTGCCTCTCCCTTCTGGCAGCAGGAGTCTCCCAGGTTGTTC
TTCTCCAGCCAGTTCCAACCTCAGGAGACAGGTCCCAAGGCCATGGGAGATCTCTCCTGTGGC
TTTGCCGGCCACTCA**TGA**GAGTGTTTTTGTGTAAAGTATTTTTTTAGAATACTGTTGACTTCT
TCATGATTTAATAACCATCCTTTGCGAAGTTTTATGAGGCTTTAGGGGAATGTCAACCCTCA
AATTTTTGTTATACTAGATGGCTTCCATTTACCCACCACTATTTTAAGGTCCCTTTATTTTT
AGGTTCAAGGTTCAATTTGACTTGAGAAAGTGCCCTTCTGCAGCTTCATTGATTTTGTTTATC
TTCCTATTAATTGTAACGATTAAAAAGAATAAGAGCACGCAGACCTCTAGGAGAATATTT
TATCCCTGGGTGCCCCTGACACATTTATGTAGTGATCCCACAAATGTGATTGTTAATTTAAA
TGTTATTCTAATATTAGTACATTCAGTTGTGATGTAATATGAATAACCAGAATCTATTTCTT
AAAAGTTTTGAGTATATTTTTCAACTAGATATTTGTATAGAAAGACTGAATAGTGATG

GGGGAATCTGCAGTAGGTCTGCCGGCGATGGAGTGGTGGGCTAGCTCGCCGCTTCGGCTCTG
GCTGCTGTTGTTCCCTCCTGCCCTCAGCGCAGGGCCGCCAGAAGGAGTCAGGTTCAAAATGGA
AAGTATTTATTGACCAAATTAACAGGTCTTTGGAGAATTACGAACCATGTTCAAGTCAAAAC
TGCAGCTGCTACCATGGTGT CATAGAAGAGGATCTAACTCCTTTCCGAGGAGGCATCTCCAG
GAAGATGATGGCAGAGGTAGTCAGACGGAAGCTAGGGACCCACTATCAGATCACTAAGAACA
GACTGTACCGGGAAAATGACTGCATGTTCCCTCAAGGTGTAGTGGTGTGAGCACTTTATT
TTGGAAGTGATCGGGCGTCTCCCTGACATGGAGATGGTGATCAATGTACGAGATTATCCTCA
GGTTCCTAAATGGATGGAGCCTGCCATCCCAGTCTTCTCCTTCAGTAAGACATCAGAGTACC
ATGATATCATGTATCCTGCTTGGACATTTTGGGAAGGGGGACCTGCTGTTTGGCCAATTTAT
CCTACAGGTCTTGGACGGTGGGACCTCTTCAGAGAAGATCTGGTAAGGTGAGCAGCACAGTG
GCCATGGAAAAAGAAAACTCTACAGCATATTTCCGAGGATCAAGGACAAGTCCAGAACGAG
ATCCTCTCATTTCTTCTGTCTCGGAAAAACCCAAAACCTTGTTGATGCAGAATACACCAAAAC
CAGGCCTGGAAATCTATGAAAGATACCTTAGGAAAGCCAGCTGCTAAGGATGTCCATCTTGT
GGATCACTGCAAATACAAGTATCTGTTTAATTTTCGAGGCGTAGCTGCAAGTTTCCGGTTTA
AACACCTCTTCCTGTGTGGCTCACTTGTTTTCCATGTTGGTGATGAGTGGCTAGAATTCTTC
TATCCACAGCTGAAGCCATGGGTTCACTATATCCCAGTCAAAACAGATCTCTCCAATGTCCA
AGAGCTGTTACAATTTGTAAAAGCAAATGATGATGTAGCTCAAGAGATTGCTGAAAGGGGAA
GCCAGTTTATTAGGAACCATTTGCAGATGGATGACATCACCTGTTACTGGGAGAACCTCTTG
AGTGAATACTCTAAATTCCTGTCTTATAATGTAACGAGAAGGAAAGGTTATGATCAAATTAT
TCCCAAATGTTGAAAACTGAACTATAGTAGTCATCATAGGACCATAGTCCTCTTTGTGGCA
ACAGATCTCAGATATCCTACGGTGAGAAGCTTACCATAAGCTTGGCTCCTATACCTTGAATA
TCTGCTATCAAGCCAAATACCTGGTTTTTCCTTATCATGCTGCACCCAGAGCAACTCTTGAGA
AAGATTTAAAATGTGTCTAATACACTGATATGAAGCAGTTCAACTTTTTGGATGAATAAGGA
CCAGAAATCGTGAGATGTGGATTTTGAACCCAACTCTACCTTTCATTTTCTTAAGACCAATC
ACAGCTTGTGCCTCAGATCATCCACCTGTGTGAGTCCATCACTGTGAAATTGACTGTGTCCA
TGTGATGATGCCCTTTGTCCCATTATTTGGAGCAGAAAATTCGTCATTTGGAAGTAGTACAA
CTCATTGCTGGAATTGTGAAATTATTCAAGGCGTGATCTCTGTCACTTTATTTTAATGTAGG
AAACCTATGGGGTTTATGAAAAATACTTGGGGATCATTCTCTGAATGGTCTAAGGAAGCGG
TAGCCATGCCATGCAATGATGTAGGAGTTCTCTTTTGTAAAACCATAAACTCTGTTACTCAG
GAGGTTTCTATAATGCCACATAGAAAGAGGCCAATTGCATGAGTAATTATTGCAATTGGATT
TCAGGTTCCCTTTTTGTGCCTTCATGCCCTACTTCTTAATGCCTCTCTAAAGCCAAA

MEWWASSPLRLWLLLFLLLPSAQGRQKESGSKWKVFIDQINRSLENYEPCCSSQNCSCYHGVIE
EDLTPFRGGISRKMMAEVVRRKLGTHYQITKNRLYRENDCMFPSRCSGVEHFILEVIGRLPD
MEMVINVRDYPQVPKWMIPAIPVFSFSKTSEYHDIMYPAWTFWEGGPVAVWPIYPTGLGRWDL
FREDLVRSAAQWPWKKKNSTAYFRGSRTSPERDPLILLSRKNPKLVD AEYTKNQAWKSMKDT
LGKPAAKDVHLVDHCKYKYLNFNFRGVAASFRFKHLFLCGSLVFHVGD EWLEFFYPQLKPVWH
YIPVKTDLSNVQELLQFVKANDDVAQEI AERGSQFIRNHLQMDDITCYWENLLSEYSKFLSY
NVTRRKGYDQIIPKMLKTEL

FIGURE 134

CACCCCTCCATTTCTCGCCATGGGCCCTGCACTGCTCCTGATCCCTGCTGCCCTCGCCTCTT
 TCATCCTGGCCTTTGGCACCGGAGTGGAGTTCGTGCGCTTTACCTCCCTTCGGCCACTTCTT
 GGAGGGATCCCGGAGTCTGGTGGTCCGGATGCCCGCCAGGGATGGCTGGCTGCCCTGCAGGA
 CCGCAGCATCCTTGCCCCCTGGCATGGGATCTGGGGCTCCTGCTTCTATTTGTTGGGCAGC
 ACAGCCTCATGGCAGCTGAAAGAGTGAAGGCATGGACATCCCGGTACTTTGGGGTCCTTCAG
 AGGTCACTGTATGTGGCCTGCACTGCCCTGGCCTTGCACTGGTGTATGCGGTACTGGGAGCC
 CATACCCAAAGGCCCTGTGTTGTGGGAGGCTCGGGCTGAGCCATGGGCCACCTGGGTGCCGC
 TCCTCTGCTTTGTGCTCCATGTATCTCCTGGCTCCTCATCTTTAGCATCCTTCTCGTCTTT
 GACTATGCTGAGCTCATGGGCCTCAAACAGGTATACTACCATGTGCTGGGGCTGGGCGAGCC
 TCTGGCCCTGAAGTCTCCCCGGGCTCTCAGACTCTTCTCCACCTGCGCCACCCAGTGTGTG
 TGGAGCTGCTGACAGTGTGTGGGTGGTGCCTACCTGGGCACGGACCGTCTCCTCCTTGCT
 TTCCTCCTTACCCTCTACCTGGGCCTGGCTCACGGGCTTGATCAGCAAGACCTCCGCTACCT
 CCGGGCCCAGCTACAAAGAAAACCTCCACCTGCTCTCTCGGCCCCAGGATGGGGAGGCAGAGT
GAGGAGCTCACTCTGGTTACAAGCCCTGTTCTTCTCCTCTCCCACTGAATTCTAAATCCTTAAC
 ATCCAGGCCCTGGCTGCTTCATGCCAGAGGCCCAAATCCATGGACTGAAGGAGATGCCCTT
 CTACTACTTGAGACTTTATTTCTCTGGGTCCAGCTCCATACCCTAAATTCTGAGTTTCAGCCA
 CTGAACTCCAAGGTCCACTTCTCACCAGCAAGGAAGAGTGGGGTATGGAAGTCATCTGTCCC
 TTCCTGTTTAGAGCATGACACTCTCCCCCTCAACAGCCTCCTGAGAAGGAAAGGATCTGCC
 CTGACCACTCCCCTGGCACTGTTACTTGCCTCTGCGCCTCAGGGGTCCCCTTCTGCACCGCT
 GGCTTCCACTCCAAGAAGGTGGACCAGGGTCTGCAAGTTCAACGGTCATAGCTGTCCCTCCA
 GGCCCCAACCTTGCTCACCCTCCCGGCCCTAGTCTCTGCACCTCCTTAGGCCCTGCCTCT
 GGGCTCAGACCCCAACCTAGTCAAGGGGATTCTCCTGCTCTTAACTCGATGACTTGGGGCTC
 CCTGCTCTCCCGAGGAAGATGCTCTGCAGGAAAATAAAAGTCAGCCTTTTTCTAAAAAAA

FIGURE 135

MAPALLLI PAALASFILAFGTGVEFVRFTSLRPLLGGIPESGGPDARQGWLAAALQDRSILAP
LAWDLGLLLLLFVGQHSLMAAERVKAWTSRYFGVLQRSLYVACTALALQLVMRYWEPIPKGPV
LWEARAEPWATWVPLLCFVLHVISWLLIFSILLVFDYAEMLGLKQVYYHVLGLGEPLALKSP
RALRLFSLRHPVCVELLTVLWVPTLGTDRLLLLAFLLTLYLGLAHGLDQQDLRYLRAQLQR
KLHLLSRPQDGEAE

Signal sequence:

amino acids 1-13

Transmembrane domains:

amino acids 58-76, 99-113, 141-159, 203-222

N-myristoylation sites:

amino acids 37-43, 42-48, 229-235

FIGURE 136

CCGAGCACAGGAGATTGCCTGCGTTTAGGAGGTGGCTGCGTTGTGGGAAAAGCTATCAAGGA
 AGAAATTGCCAAACCATGTCTTTTTTTCTGTTTTTCAGAGTAGTTCACAACAGATCTGAGTGT
 TTTAATTAAGCATGGAATACAGAAAACAACAAAAAACTTAAGCTTTAATTTATCTGGAATT
 CCACAGTTTTCTTAGCTCCCTGGACCCGGTTGACCTGTTGGCTCTTCCCCTGGCTGCTCTA
 TCACGTGGTGTCTCCGACTACTCACCCCGAGTGTAAGAACCTTCGGCTCGCGTGCTTCTG
 AGCTGCTGTGGATGGCCTCGGCTCTCTGGACTGTCCTTCCGAGTAGGATGTCACTGAGATCC
 CTCAAATGGAGCCTCCTGCTGCTGTCACTCCTGAGTTTCTTTGTGATGTGGTACCTCAGCCT
 TCCCCACTACAATGTGATAGAACGCGTGAAGTGGATGTACTTCTATGAGTATGAGCCGATTT
 ACAGACAAGACTTTCACTTCACACTTCGAGAGCATTCAAAGTCTCTCATCAAAATCCATTT
 CTGGTCATTCTGGTGACCTCCCACCCCTCAGATGTGAAAGCCAGGCAGGCCATTAGAGTTAC
 TTGGGGTGAAAAAAGTCTTGGTGGGGATATGAGGTTCTTACATTTTTCTTATTAGGCCAAG
 AGGCTGAAAAGGAAGACAAAATGTTGGCATTGTCCTTAGAGGATGAACACCTTCTTTATGGT
 GACATAATCCGACAAGATTTTTTAGACACATATAATAACCTGACCTTGAAAACCATTATGGC
 ATTCAGGTGGGTAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT
 TTTTCATCAATACTGGCAATTTAGTGAAGTATCTTTTAAACCTAAACCACTCAGAGAAGTTT
 TTCACAGGTTATCCTCTAATTGATAATTATTCCTATAGAGGATTTTACCAAAAAACCCATAT
 TTCTTACCAGGAGTATCCTTTCAAGGTGTTCCCTCCATACTGCAGTGGGTTGGGTTATATAA
 TGTCCAGAGATTTGGTGCCAAGGATCTATGAAATGATGGGTACGTAAGAACCCATCAAGTTT
 GAAGATGTTTATGTCGGGATCTGTTTGAATTTATTAAGTGAACATTCATATTCCAGAAGA
 CACAAATCTTTTCTTTCTATATAGAATCCATTTGGATGTCTGTCAACTGAGACGTGTGATTG
 CAGCCCATGGCTTTTCTTCCAAGGAGATCATCACTTTTGGCAGGTCATGCTAAGGAACACC
 ACATGCCATTATTAAGTCTTCACTTCTACAAAAGCCTAGAAGGACAGGATACCTTGTGGAAA
 GTGTTAAATAAAGTAGGTACTGTGGAAAATTCATGGGGAGGTCAGTGTGCTGGCTTACACTG
 AACTGAAACTCATGAAAACCCAGACTGGAGACTGGAGGGTTACACTTGTGATTTATTAGTC
 AGGCCCTTCAAAGATGATATGTGGAGGAATTAAATATAAAGGAATTGGAGGTTTTTGCTAAA
 GAAATTAATAGGACCAAACAATTTGGACATGTCATTCTGTAGACTAGAATTTCTTAAAGGG
 TGTTACTGAGTTATAAGCTCACTAGGCTGTAAAACAAAACAATGTAGAGTTTTATTATTG
 AACAAATGTAGTCACTTGAAGGTTTTGTGTATATCTTATGTGGATTACCAATTTAAAAATATA
 TGTTAGTTCTGTGTCAAAAACTTCTTCACTGAAGTTATACTGAACAAAATTTTACCTGTTTT
 TGGTCATTTATAAAGTACTTCAAGATGTTGCAGTATTTACAGTTATTATTATTTAAATTA
 CTTCAACTTTGTGTTTTTAAATGTTTTGACGATTTCAATACAAGATAAAAAGGATAGTGAAT
 CATTCTTTACATGCAACATTTTCCAGTTACTTAACTGATCAGTTTATTATTGATACATCAC
 TCCATTAATGTAAAGTCATAGGTCATTATTGCATATCAGTAATCTCTTGGACTTTGTAAAT
 ATTTTACTGTGGTAATATAGAGAAGAATTAAAGCAAGAAAATCTGAAAA

FIGURE 137

MASALWTVLPSRMSLRSLKWSLLLLSLLSFFVMWYLSLPHYNVIERVNWMYFYEYEPYRQD
FHFTLREHSNCSHQNPFLVILVTSHPSDVKARQAIRVTWGEKKSWWGYEVLTFLLGQEA EK
EDKMLALSLEDEHLLYGDIIRQDFLDTYNNLTLKTIMAFRWVTEFCPNAKYVMKTDTDVFIN
TGNLVKYLLNLNHSEKFFTGYPLIDNYSYRGFYQKTHISYQEYPFKVFPPYCSGLGYIMSRD
LVPRIYEMMGHVKPIKFEDVYVGICLNLLKVNHIHPEDTNLFFLYRIHLDVCQLRRVIAAHG
FSSKEIITFWQVMLRNTTCHY

T02T T " 3T T 6660

FIGURE 138

CCTCTGTCCACTGCTTTTCGTGAAGACAAGATGAAGTTCACAATTGTCTTTGCTGGACTTCTT
GGAGTCTTTCTAGCTCCTGCCCTAGCTAACTATAATATCAACGTCAATGATGACAACAACAA
TGCTGGAAGTGGGCAGCAGTCAGTGAGTGTCAACAATGAACACAATGTGGCCAATGTTGACA
ATAACAACGGATGGGACTCCTGGAATTCCATCTGGGATTATGGAAATGGCTTTGCTGCAACC
AGACTCTTTCAAAAGAAGACATGCATTGTGCACAAAATGAACAAGGAAGTCATGCCCTCCAT
TCAATCCCTTGATGCACTGGTCAAGGAAAAGAAGCTTCAGGGTAAGGGACCAGGAGGACCAC
CTCCCAAGGGCCTGATGTACTCAGTCAACCCAAACAAAGTCGATGACCTGAGCAAGTTCGGA
AAAAACATTGCAAACATGTGTTCGTGGGATTCCAACATACATGGCTGAGGAGATGCAAGAGGC
AAGCCTGTTTTTTTTACTCAGGAACGTGCTACACGACCAGTGTACTATGGATTGTGGACATTT
CCTTCTGTGGAGACACGGTGGAGAACTAAACAATTTTTTAAAGCCACTATGGATTTAGTCAT
CTGAATATGCTGTGCAGAAAAAATATGGGCTCCAGTGGTTTTTACCATGTCATTCTGAAATT
TTTCTCTACTAGTTATGTTTGATTTCCTTAAGTTTCAATAAAATCATTTAGCATTGAAAAAAA

FIGURE 139

MKFTIVFAGLLGVFLAPALANYNINVNDDNNNAGSGQQSVSVNNEHNVANVDNNNGWDSWNS
IWDYGNGFAATRLFQKKTCTIVHKMNKEVMPSIQSLDALVKEKKLQKGPGGPPPKGLMYSVN
PNKVDDLKFGKNIANMCRGIPTYMAEEMQEASLFFYSGTCYTTSVLWIVDISFCGDTVEN

Signal Peptide:

amino acids 1-20

N-myristoylation Sites:

amino acids 67-72, 118-123, 163-168

Flavodoxin protein homology:

amino acids 156-174

Parameter	Value	Unit
Initial concentration	1.0	g/L
Initial pH	7.0	
Temperature	25	°C
Time	0, 1, 2, 4, 8, 16, 32, 64, 128, 256, 512, 1024, 2048, 4096, 8192, 16384, 32768, 65536, 131072, 262144, 524288, 1048576, 2097152, 4194304, 8388608, 16777216, 33554432, 67108864, 134217728, 268435456, 536870912, 1073741824, 2147483648, 4294967296, 8589934592, 17179869184, 34359738368, 68719476736, 137438953472, 274877906944, 549755813888, 1099511627776, 2199023255552, 4398046511104, 8796093022208, 17592186044416, 35184372088832, 70368744177664, 140737488355328, 281474976710656, 562949953421312, 1125899906842624, 2251799813685248, 4503599627370496, 9007199254740992, 18014398509481984, 36028797018963968, 72057594037927936, 144115188075855872, 288230376151711744, 576460752303423488, 1152921504606846976, 2305843009213693952, 4611686018427387904, 9223372036854775808, 18446744073709551616, 36893488147419103232, 73786976294838206464, 147573952589676412928, 295147905179352825856, 590295810358705651712, 1180591620717411303424, 2361183241434822606848, 4722366482869645213696, 9444732965739290427392, 18889465931478580854784, 37778931862957161709568, 75557863725914323419136, 151115727451828646838272, 302231454903657293676544, 604462909807314587353088, 1208925819614629174706176, 2417851639229258349412352, 4835703278458516698824704, 9671406556917033397649408, 19342813113834066795298816, 38685626227668133590597632, 77371252455336267181195264, 154742504910672534362390528, 309485009821345068724781056, 618970019642690137449562112, 1237940039285380274899124224, 2475880078570760549798248448, 4951760157141521099596496896, 9903520314283042199192993792, 19807040628566084398385987584, 39614081257132168796771975168, 79228162514264337593543950336, 158456325028528675187087900672, 316912650057057350374175801344, 633825300114114700748351602688, 1267650600228229401496703205376, 2535301200456458802993406410752, 5070602400912917605986812821504, 10141204801825835211973625643008, 20282409603651670423947251286016, 40564819207303340847894502572032, 81129638414606681695789005144064, 162259276829213363391578010288128, 324518553658426726783156020576256, 649037107316853453566312041152512, 1298074214633706907132624082305024, 2596148429267413814265248164610048, 5192296858534827628530496329220096, 10384593717069655257060992658440192, 20769187434139310514121985316880384, 41538374868278621028243970633760768, 83076749736557242056487941267521536, 166153499473114484112975882535043072, 332306998946228968225951765070086144, 664613997892457936451903530140172288, 1329227995784915872903807060280344576, 2658455991569831745807614120560689152, 5316911983139663491615228241121378304, 10633823966279326983230456482242756608, 21267647932558653966460912964485513216, 42535295865117307932921825928971026432, 85070591730234615865843651857942052864, 170141183460469231731687303715884105728, 340282366920938463463374607431768211456, 680564733841876926926749214863536422912, 1361129467683753853853498429727072845824, 2722258935367507707706996859454145691648, 5444517870735015415413993718908291383296, 10889035741470030830827987437816582766592, 21778071482940061661655974875633165533184, 43556142965880123323311949751266331066368, 87112285931760246646623899502532662132736, 174224571863520493293247799005065324265472, 348449143727040986586495598010130648530944, 696898287454081973172991196020261297061888, 1393796574908163946345982392040522594123776, 2787593149816327892691964784081045188247552, 5575186299632655785383929568162090376495104, 11150372599265311570767859136324180752990208, 22300745198530623141535718272648361505980416, 44601490397061246283071436545296723011960832, 89202980794122492566142873090593446023921664, 178405961588244985132285746181186892047843328, 356811923176489970264571492362373784095686656, 713623846352979940529142984724747568191373312, 1427247692705959881058285969449495136382746624, 2854495385411919762116571938898990272765493248, 5708990770823839524233143877797980545530986496, 11417981541647679048466287755595961091061972992, 2283596308329	

Parameter	Value	Unit
Initial concentration	1.0	g/L
Initial pH	7.0	
Temperature	25	°C
Time	0, 1, 2, 4, 8, 16, 32, 64, 128, 256, 512, 1024, 2048, 4096, 8192, 16384, 32768, 65536, 131072, 262144, 524288, 1048576, 2097152, 4194304, 8388608, 16777216, 33554432, 67108864, 134217728, 268435456, 536870912, 1073741824, 2147483648, 4294967296, 8589934592, 17179869184, 34359738368, 68719476736, 137438953472, 274877906944, 549755813888, 1099511627776, 2199023255552, 4398046511104, 8796093022208, 17592186044416, 35184372088832, 70368744177664, 140737488355328, 281474976710656, 562949953421312, 1125899906842624, 2251799813685248, 4503599627370496, 9007199254740992, 18014398509481984, 36028797018963968, 72057594037927936, 144115188075855872, 288230376151711744, 576460752303423488, 1152921504606846976, 2305843009213693952, 4611686018427387904, 9223372036854775808, 18446744073709551616, 36893488147419103232, 73786976294838206464, 147573952589676412928, 295147905179352825856, 590295810358705651712, 1180591620717411303424, 2361183241434822606848, 4722366482869645213696, 9444732965739290427392, 18889465931478580854784, 37778931862957161709568, 75557863725914323419136, 151115727451828646838272, 302231454903657293676544, 604462909807314587353088, 1208925819614629174706176, 2417851639229258349412352, 4835703278458516698824704, 9671406556917033397649408, 19342813113834066795298816, 38685626227668133590597632, 77371252455336267181195264, 154742504910672534362390528, 309485009821345068724781056, 618970019642690137449562112, 1237940039285380274899124224, 2475880078570760549798248448, 4951760157141521099596496896, 9903520314283042199192993792, 19807040628566084398385987584, 39614081257132168796771975168, 79228162514264337593543950336, 158456325028528675187087900672, 316912650057057350374175801344, 633825300114114700748351602688, 1267650600228229401496703205376, 2535301200456458802993406410752, 5070602400912917605986812821504, 10141204801825835211973625643008, 20282409603651670423947251286016, 40564819207303340847894502572032, 81129638414606681695789005144064, 162259276829213363391578010288128, 324518553658426726783156020576256, 649037107316853453566312041152512, 1298074214633706907132624082305024, 2596148429267413814265248164610048, 5192296858534827628530496329220096, 10384593717069655257060992658440192, 20769187434139310514121985316880384, 41538374868278621028243970633760768, 83076749736557242056487941267521536, 166153499473114484112975882535043072, 332306998946228968225951765070086144, 664613997892457936451903530140172288, 1329227995784915872903807060280344576, 2658455991569831745807614120560689152, 5316911983139663491615228241121378304, 10633823966279326983230456482242756608, 21267647932558653966460912964485513216, 42535295865117307932921825928971026432, 85070591730234615865843651857942052864, 170141183460469231731687303715884105728, 340282366920938463463374607431768211456, 680564733841876926926749214863536422912, 1361129467683753853853498429727072845824, 2722258935367507707706996859454145691648, 5444517870735015415413993718908291383296, 10889035741470030830827987437816582766592, 21778071482940061661655974875633165533184, 43556142965880123323311949751266331066368, 87112285931760246646623899502532662132736, 174224571863520493293247799005065324265472, 348449143727040986586495598010130648530944, 696898287454081973172991196020261297061888, 1393796574908163946345982392040522594123776, 2787593149816327892691964784081045188247552, 5575186299632655785383929568162090376495104, 11150372599265311570767859136324180752990208, 22300745198530623141535718272648361505980416, 44601490397061246283071436545296723011960832, 89202980794122492566142873090593446023921664, 178405961588244985132285746181186892047843328, 356811923176489970264571492362373784095686656, 713623846352979940529142984724747568191373312, 1427247692705959881058285969449495136382746624, 2854495385411919762116571938898990272765493248, 5708990770823839524233143877797980545530986496, 11417981541647679048466287755595961091061972992, 2283596308329	

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FIGURE 141

MNDSLRTNVFVRFQPETIACACIYLAARALQIPLPTRPHWELLFGTTEEEIQEICIETLRLY
TRKKPNYELLEKEVEKRKVALQEAKLKAKGLNPDGTPALSTLGGFSPASKPSSPREVKAEEK
SPISINVKTVKKEPEDRQQASKSPYNGVRKDSKRSRNSRSASRSRSTRSRSRSHTPRRHYN
NRRSRSGTYSSRSRSTRSHSESPRRHHNHGSPHLKAKHTRDDLKSSNRHGHKRKKSRSRSQ
SKSRDHSDAAKKHRHERGHHRDRRERSRSFERSHKS KHHGGSRS GHGRHR

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FIGURE 142

TGGGGATAAAGGAAAAATGGTCAGGTATTAATGGCTTAAAGATTATTGGAAGGGGTTTATCA
TTTTTTGAANNTATTCGGGTCANAATTGNCTTTGAAAAGCATTGCTTTTTACAGAAATATAT
TANCTTTTTAGAGTAATTTCTAGTTTGGATTGTAATATGAAATTATTTAAAAGGGCTTCGCT
CATATATAGGAAAATCGCATATGGTCCTAGTATTAAATTNTTATTGCTTACTGATTTTTTTG
AGTTAAGAGTTGTTATATGNTAGAATATGAGGATGTGAATATAAATAAGAGAAGAAAAAGA
ATAAAGTAGATTGAGTCTCCAATTTTATGTAAGCTTCAGAAGAAGTGGTTTGTTTACATGCA
AGCTTATAGTTGAAATATTTTTTCAGGAATTACATGAATGACAGTCTTCGAACCAATGTGTTT
GTTCGATTTCAACCAGAGANTATAGCATGTGCTTGCATCTACCTTGCAGNTAGAGCACTTCA
GATTCCGTTGCCAACTNGTCCCCATTGGTTTCTTCTTTTTGGTACTACAGAAGAGGAAATCC
AGGAAATNTGCATAGAAACACTTAGGCCTTTATACCAGAAAAAAGCCAACTATGAATTACTG
GAAAAAGAAGTAGAAAAAAGAAAAGTAGCCTTACAAGAAGCCNAATTAAAAGCAAAGGGATT
GAATCCGGATGGAAGTCCAGCCCTTTCAACCCTGGGTGGATTTTCTCC

FIGURE 143

GGCACGAGGCCTCGTGCCAAGCTTGGCACGAGGGTGCACCGCGTTCTCGCACGCGT**CATGGC**
GGTCCTCGGAGTACAGCTGGTGGTGACCCTGCTCACTGCCACCCTCATGCACAGGCTGGCGC
CACACTGCTCCTTCGCGCGCTGGCTGCTCTGTAACGGCAGTTTGTTCGATACAAGCACCCG
TCTGAGGAGGAGCTTCGGGCCCTGGCGGGGAAGCCGAGGCCAGAGGCAGGAAAGAGCGGTG
GGCCAATGGCCTTAGTGAGGAGAAGCCACTGTCTGTGCCCCGAGATGCCCCGTTCCAGCTGG
AGACCTGCCCCCTCACGACCGTGGATGCCCTGGTCCTGCGCTTCTTCCTGGAGTACCACTGG
TTTGTGGACTTTGCTGTGTACTCGGGCGGCGTGTACCTCTTCACAGAGGCCTACTACTACAT
GCTGGGACCAGCCAAGGAGACTAACATTGCTGTGTTCTGGTGCCTGCTCACGGTGACCTTCT
CCATCAAGATGTTCTTGACAGTGACACGGCTGTACTTCAGCGCCGAGGAGGGGGGTGAGCGC
TCTGTCTGCCTCACCTTTGCCTTCTCTTCCTGCTGCTGGCCATGCTGGTGCAAGTGGTGCG
GGAGGAGACCCTCGAGCTGGGCCTGGAGCCTGGTCTGGCCAGCATGACCCAGAACTTAGAGC
CACTTCTGAAGAAGCAGGGCTGGGACTGGGCGCTTCTGTGGCCAAGCTGGCTATCCGCGTG
GGACTGGCAGTGGTGGGCTCTGTGCTGGGTGCCTTCTCACCTTCCCAGGCCTGCGGCTGGC
CCAGACCCACCGGGACGCACTGACCATGTCGGAGGACAGACCCATGCTGCAGTTCCTCCTGC
ACACCAGCTTCCTGTCTCCCCGTTCATCCTGTGGCTCTGGACAAAGCCCATTGACGGGAC
TTCCTGCACCAGCCGCCGTTTGGGGAGACGCGTTTCTCCCTGCTGTCCGATTCTGCCTTCGA
CTCTGGGCGCCTCTGGTTGCTGGTGGTGTGTGCCTGCTGCGGCTGGCGGTGACCCGGCCCC
ACCTGCAGGCCTACCTGTGCCTGGCCAAGGCCCGGGTGGAGCAGCTGCGAAGGGAGGCTGGC
CGCATCGAAGCCCGTGAAATCCAGCAGAGGGTGGTCCGAGTCTACTGCTATGTGACCGTGGT
GAGCTTGACGTACCTGACGCCGCTCATCCTCACCTCAACTGCACACTTCTGCTCAAGACGC
TGGGAGGCTATTCTGGGGCCTGGGCCCAGCTCCTCTACTATCCCCGACCCATCCTCAGCC
AGCGCTGCCCCCATCGGCTCTGGGGAGGACGAAGTCCAGCAGACTGCAGCGCGGATTGCCGG
GGCCTGGGTGGCCTGCTTACTCCCCCTCTTCTCCGTGGCGTCTTGGCCTACCTCATCTGGT
GGACGGCTGCCTGCCAGCTGCTCGCCAGCCTTTTCGGCCTCTACTTCCACCAGCACTTGGCA
GGCTCC**TAG**CTGCCTGCAGACCCTCCTGGGGCCCTGAGGTCTGTTCTGGGGCAGCGGGACA
CTAGCCTGCCCCCTCTGTTTGCGCCCCCGTGTCCCCAGCTGCAAGGTGGGGCCGGACTCCCC
GGCGTTCCCTTCACCACAGTGCCTGACCCGCGGCCCCCTTGGACGCCGAGTTTCTGCCTCA
GAACTGTCTCTCCTGGGCCCAGCAGCATGAGGGTCCCGAGGCCATTGTCTCCGAAGCGTATG
TGCCAGGTTTGAGTGGCGAGGGTGATGCTGGCTGCTCTTCTGAACAAATAAAGGAGCATGCC
GATTTTAA

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FIGURE 144

MAVLGVQLVVTLLTATLMHRLAPHCSFARWLLCNGSLFRYKHPSEELRALAGKPRPRGRKE
RWANGLSEEKPLSVPRDAPFQLETCPLETTVDALVLRFFLEYQWFVDFAVYSGGVYLFTEAYY
YMLGPAKETNIAVFWCLLTVTFSIKMFLTVTRLYFSAEEGGERSVCLTFAFLFLLLAMLVQV
VREETLELGLPGLASMTQNLPLLLKKQGDWALPVAKLAIRVGLAVVGSVLGAFLTFPGLR
LAQTHRDALTMSEDRPMLQFLLHTSFLSPLFILWLWTKPIARDFLHQPPFGETRFSLLSDSA
FDSGRLWLLVVLCLLRLAVTRPHLQAYLCLAKARVEQLRREAGRIEAREIQQRVVRVYCYVT
VVSLQYLTPILTLNCTLLKTLGGYSWGLGPAPLLSPDPSSASAAPIGSGEDEVQQTAAARI
AGALGGLLTPLFLRGVLAYLIWWTAACQLLASLFGLYFHQHLGS

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FIGURE 145

CGTTNGCACGCGTCAATGGCGGTCCCTCGGAGTACAGCTGGTGGTGACCCTGCTCACTGCCAC
CCTCATGCACAGGCTGGCGCCACACTGCTCCTTCGCGCGCTGGCTGCTCTGTAAACGGCAGTT
TGTTCCGATACAAGCACCCGTNTTGAGGAGGAGCTTCGGGCCCTGGCGGGGAAGCCGAGGCC
CAGAGGCAGGAAAGAGCGGTGGGCCAATGGCCTTAGTGAGGAGAAGCCACTGTCTGTGCCCC
GAGATGCCCCGTTCCAGCTGGAGACCTGCCCCCTCACGACCGTGGATGCCCTGGTCCTGCGC
TTCTTCCTGGAGTACCAGTGGTTTGTGGACTTTGCTGTGTACTCGGGCGGCGTGTACCTCTT
CACAGAGGCCTACTACTACATGCTGGGACCAGCCAAGGAGACTAACATTGCTGTGTTCTGGT
GCCTGCTCACAGTGACCTTCTCCATCAAGATGTTCCCTGACAGTGACACGGCTGTACTTCAGC
GCCGAGGAGGGGGGTGAGCGCTCTGTCTGCCTCACCTTTGCCTTCCTCTTCCTGCTGCTGGC
CATGCTGGTGCAAGCG

FIGURE 146

GGTTCCTACATCCTCTCATCTGAGAATCAGAGAGCATAATCTTCTTACGGGCCCCGTGATTTATTAACGTGGCTT
 AATCTGAAGGTTCTCAGTCAAATTCTTTGTGATCTACTGATTGTGGGGGCATGGCAAGGTTTGCTTAAAGGAGC
 TTGGCTGGTTTGGGCCCTTGTAGCTGACAGAAGGTGGCCAGGGAGAATGCAGCACACTGCTCGGAGAATGAAGG
 CGCTTCTGTTGCTGGTCTTGCCTTGGCTCAGTCCTGCTAACTACATTGACAATGTGGGCAACCTGCACTTCCTG
 TATTCAGAACTCTGTAAAGGTGCCTCCCACTACGGCCTGACCAAAGATAGGAAGAGGCGCTCACAAGATGGCTG
 TCCAGACGGCTGTGCGAGCCTCACAGCCACGGCTCCCTCCCCAGAGGTTTCTGCAGCTGCCACCATCTCCTTAA
 TGACAGACGAGCCTGGCCTAGACAACCCTGCCTACGTGTCTCGGCAGAGGACGGGCAGCCAGCAATCAGCCCA
 GTGGACTCTGGCCGGAGCAACCGAACTAGGGCACGGCCCTTTGAGAGATCCACTATTAGAAGCAGATCATTTAA
 AAAAATAAATCGAGCTTTGAGTGTCTTCTGAAGGACAAAGAGCGGGAGTGCAGTTGCCAACCATGCCGACCAGG
 GCAGGGAAAATTCTGAAAACACCACTGCCCTGAAGTCTTTCCAAGGTTGTACCACCTGATCCAGATGGTGAA
 ATTACCAGCATCAAGATCAATCGAGTAGATCCCAGTGAAAGCCTCTCTATTAGGCTGGTGGGAGGTAGCGAAAC
 CCCACTGGTCCATATCATTATCCAACACATTTATCGTGATGGGGTGATCGCCAGAGACGGCCGGCTACTGCCAG
 GAGACATCATTCTAAAGGTCAACGGGATGGACATCAGCAATGTCCCTCACAACCTACGCTGTGCGTCTCCTGCCG
 CAGCCCTGCCAGGTGCTGTGGCTGACTGTGATGCGTGAACAGAAGTTCGCGAGCAGGAACAATGGACAGGCCCC
 GGATGCCCTACAGACCCCGAGATGACAGCTTTTCATGTGATTCTCAACAAAAGTAGCCCCGAGGAGCAGCTTGAA
 TAAACTGGTGCGCAAGGTGGATGAGCCTGGGGTTTTTCATCTTCAATGTGCTGGATGGCGGTGTGGCATATCGA
 CATGGTCAGCTTGAGGAGAATGACCGTGTGTTAGCCATCAATGGACATGATCTTCGATATGGCAGCCCAGAAAG
 TGCGGCTCATCTGATTGAGGCCAGTGAAAGACGTGTTACCTCGTGTGTCGCGCCAGGTTCCGCGAGCGGAGCC
 CTGACATCTTTCAGGAAGCCGGCTGGAACAGCAATGGCAGCTGGTCCCCAGGGCCAGGGGAGAGGAGCAACACT
 CCCAAGCCCCCTCCATCCTACAATTACTTGTGATGAGAAGGTGGTAAATATCCAAAAAGACCCCGGTGAATCTCT
 CGGCATGACCGTCGCGAGGGGGAGCATCACATAGAGAATGGGATTTGCCTATCTATGTCATCAGTGTGAGCCCCG
 GAGGAGTCATAAGCAGAGATGGAAGAATAAAAAACAGGTGACATTTTGTGAAATGTGGATGGGGTCGAACTGACA
 GAGGTGAGCCGGAGTGAGGCAGTGGCATTATTGAAAAGAACATCATCCTCGATAGTACTCAAAGCTTTGGAAGT
 CAAAGAGTATGAGCCCCAGGAAGACTGCAGCAGCCCAGCAGCCCTGGACTCCAACCACAACATGGCCCCACCCA
 GTGACTGGTCCCCATCCTGGGTGATGTGGCTGGAATTACCACGGTGTGTTGATAACTGTAAAGATATTGTATTA
 CGAAGAAACACAGCTGGAAGTCTGGGCTTCTGCATTGTAGGAGGTTATGAAGAATACAATGGAAACAAACCTTT
 TTTTCATCAAATCCATTGTTGAAGGAACACCAGCATAACAATGATGGAAGAATTAGATGTGGTGATATTCTTCTTG
 CTGTCAATGGTAGAAGTACATCAGGAATGATACATGCTTGCTTGGCAAGACTGCTGAAAGAACTTAAAGGAAGA
 ATTACTCTAACTATTGTTTCTTGGCCTGGCACTTTTTTTATAGAAATCAATGATGGGTGAGAGGAAAACAGAAAAA
 TCACAAATAGGCTAAGAAGTTGAAACACTATATTTATCTTGTGAGTTTTTATATTTAAAGAAAGAATACATTGT
 AAAAATGTGAGGAAAAGTATGATCATCTAATGAAAGCCAGTTACACCTCAGAAAAATGATTCAAAAAAATTA
 AAACCTACTAGTTTTTTTTTCAGTGTGGAGGATTTCTCATTACTCTACAACATTGTTTATATTTTTTCTATTCAAT
 AAAAGCCCTAAAAACAATAAAATGATTGATTTGTATACCCCACTGAATTCAGCTGATTTAAATTTAAATTTT
 GGTATATGCTGAAGTCTGCCAAGGGTACATTATGGCCATTTTTTAATTTACAGCTAAAATATTTTTTAAATGCA
 TTGCTGAGAAACGTTGCTTTTCATCAAACAAGAATAAATATTTTTTCAGAAAGTTAAA

MKALLLLVLPWLSPANYIDNVGNLHFLYSELCKGASHYGLTKDRKRRSQDGCPCDGCASLTAT
APSPEVSAAATISLMTDEPGLDNPAYVSSAEDGQPAISPVDSGRSNRTRARPFFERSTIRSR
FKKINRALSVLRRTKSGSAVANHADQGRESENTTAPEVFPRLYHLIPDGEITSIKINRVP
SESLSIRLVGGSETPLVHIIIQHIYRDGVIARDGRLLPGDIILKVNMDISNVPHNYAVRLL
RQPCQVLWLTVMREQKFRSRNNGQAPDAYRPRDDSFHVILNKSSPEEQLGIKLVKRVDEPGV
FIFNVLDGGVAYRHHGLEENDRVLAINGHDLRYGSPESAHLIQASERRVHLVVSQRQR
PDIHQEAGWNSNGSWSPGPGERSNTPKPLHPTITCHEKVNIQKDPGESLGMTVAGGASHRE
WDLPIYVISVEPGGVISRDGRIKTGDILLNVDGVELTEVSRSEAVALLKRTSSSIVLKALEV
KEYEPQEDCSSPAALDSNHNMAPSPDWSPSWMWLELPRCLYNCKDIVLRRNTAGSLGFCIV
GGYEEYNGNKPFFIKSIVEGTPAYNDGRIRCGDILLAVNGRSTSGMIHACLARLLKELKGRI
TLTIVSWPGTFL

FIGURE 148

CCAAAGTGATCATTTGAAAAAGAGATATCCACATCTTCAAGCCCATATAAAGGATAGAAGCT
GCACAGGGCAGCTTTACTTACTCCAGCACCTTCCTCTCCCAGGCAA**ATG**GTGCTGACCATCT
TTGGGATACAATCTCATGGATACGAGGTTTTTAACATCATCAGCCCAAGCAACAATGGTGGC
AATGTTTCAGGAGACAGTGACAATTGATAATGAAAAAATACCGCCATCGTTAACATCCATGC
AGGATCATGCTCTTCTACCACAATTTTTGACTATAAACATGGCTACATTGCATCCAGGGTGC
TCTCCCGAAGAGCCTGCTTTATCCTGAAGATGGACCATCAGAACATCCCTCCTCTGAACAAT
CTCCAATGGTACATCTATGAGAAACAGGCTCTGGACAACATGTTCTCCAACAAATACACCTG
GGTCAAGTACAACCCTCTGGAGTCTCTGATCAAAGACGTGGATTGGTTCCTGCTTGGGTAC
CCATTGAGAACTCTGCAAACATATCCCTTTGTATAAGGGGGAAGTGGTTGAAAACACACAT
AATGTCGGTGCTGGAGGCTGTGCAAAGGCTGGGCTCCTGGGCATCTTGGGAATTTCAATCTG
TGCAGACATTCATGTT**TAG**GATGATTAGCCCTCTTGTTTTATCTTTTCAAAGAAATACATCC
TTGGTTTACACTCAAAGTCAAATTAAATTCTTTCCCAATGCCCCAACTAATTTTGAGATTC
AGTCAGAAAATATAAATGCTGTATTTATA

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FIGURE 149

MKILVAFLVVLTI FGIQSHGYEVFNII SP SNNGGNVQETVTIDNEKNTAIVNIHAGSCSSTT
IFDYKHGYIASRVLSRRACFILKMDHQNIPPLNNLQWYIYEKQALDNMFSNKYTWVKYNPLE
SLIKDVDWFLLGSPIEKLCKHIPPLYKGEVVENTHNVGAGGCAKAGLLGILGISICADIHV

NOT PRESENT

GGCACGAGCCAGGAAC TAGGAGGTTCTCACTGCCCGAGCAGAGGCCCTACACCCACCGAGGC
ATGGGGCTCCCTGGGCTGTTCTGCTTGCCGTGCTGGCTGCCAGCAGCTTCTCCAAGGCACG
GGAGGAAGAAATTACCCCTGTGGTCTCCATTGCCTACAAAGTCCTGGAAGTTTTCCCCAAAG
GCCGCTGGGTGCTCATAACCTGCTGTGCACCCAGCCACCACCGCCCATCACCTATTCCCTC
TGTGGAACCAAGAACATCAAGGTGGCCAAGAAGGTGGTGAAGACCCACGAGCCGGCCTCCTT
CAACCTCAACGTCACACTCAAGTCCAGTCCAGACCTGCTCACCTACTTCTGCCGGGCGTCCT
CCACCTCAGGTGCCCATGTGGACAGTGCCAGGCTACAGATGCACTGGGAGCTGTGGTCCAAG
CCAGTGTCTGAGCTGCGGGCCAACTTCACTCTGCAGGACAGAGGGGCAGGCCCCAGGGTGGA
GATGATCTGCCAGGCGTCCTCGGGCAGCCACCTATCACCAACAGCCTGATCGGGAAGGATG
GGCAGGTCCACCTGCAGCAGAGACCATGCCACAGGCAGCCTGCCAACTTCTCCTTCTTGCCG
AGCCAGACATCGGACTGGTTCTGGTGCCAGGCTGCAAACAACGCCAATGTCCAGCACAGCGC
CCTCACAGTGGTGCCCCCAGGTGGTGACCAGAAGATGGAGGACTGGCAGGGTCCCCTGGAGA
GCCCCATCCTTGCCCTTGCCGCTCTACAGGAGCACCCGCCGTCTGAGTGAAGAGGAGTTTGGG
GGGTTCAGGATAGGGAATGGGGAGGTGAGAGGACGCAAAGCAGCAGCCATG**TAG**AATGAACC
GTCCAGAGAGCCAAGCACGGCAGAGGACTGCAGGCCATCAGCGTGCACTGTTCGTATTTGGA
GTTTCATGCAAAATGAGTGTGTTTTAGCTGCTCTTGCCACAAAAAAAAAAAAAAAAAAAAAA

MGLPGLFCLAVLAASSFSKAREEEITPVVSIAYKVLEVPKGRWVLITCCAPQPPPPITYSL
CGTKNIKVAKKVVKTHEPASFNLNVTCLKSSPDLLTYFCRASSTSGAHVDSARLQMHWELWSK
PVSELNANFTLQDRGAGPRVEMICQASSGSPITNSLIGKDGQVHLQQRPCHRQPANFSFLP
SQTSDWFWCQAANNANVQHSALTVVPPGGDQKMEDWQGPLESPILALPLYRSTRRLSEEEFG
GFRIGNGEVRGRKAAAM

amino acids 1-18

amino acids 86-89, 132-135, 181-184

FIGURE 152

GGTCTTAAATGGCAGCAGCCGCCGCTACCAAGATCCTTCTGTGCCTCCCGCTTCTGCTCCTG
CTGTCCGGGCTGGTCCCGGGCTGGGCGAGCCGACCCTCACTCTCTTTGCTATGACATCACCGT
CATCCCTAAGTTCAGACCTGGACCACGGTGGTGTGCGGTTCAAGGCCAGGTGGATGAAAAGA
CTTTTCTTCACTATGACTGTGGCAACAAGACAGTCACACCTGTCAGTCCCCTGGGGAAGAAA
CTAAATGTCACAACGGCCTGGAAAGCACAGAACCCAGTACTGAGAGAGGTGGTGGACATACT
TACAGAGCAACTGCGTGACATTCACTGGAGAATTACACACCCAAGGAACCCCTCACCCCTGC
AGGCAAGGATGTCTTGTGAGCAGAAAGCTGAAGGACACAGCAGTGGATCTTGGCAGTTCAGT
TTCGATGGGCAGATCTTCCTCCTCTTTGACTCAGAGAAGAGAATGTGGACAACGGTTCATCC
TGGAGCCAGAAAGATGAAAGAAAAGTGGGAGAATGACAAGGTTGTGGCCATGTCCTTCCATT
ACTTCTCAATGGGAGACTGTATAGGATGGCTTGAGGACTTCTTGATGGGCATGGACAGCACC
CTGGAGCCAAGTGCAGGAGCACCCTCGCCATGTCCTCAGGCACAACCCAACTCAGGGCCAC
AGCCACCACCCTCATCCTTTGCTGCCTCCTCATCATCCTCCCCTGCTTCATCCTCCCTGGCA
TCTGAGGAGAGTCCTTTAGAGTGACAGGTTAAAGCTGATACCAAAGGCTCCTGTGAGCACG
GTCTTGATCAAACCTCGCCCTTCTGTCTGGCCAGCTGCCCACGACCTACGGTGTATGTCCAGT
GGCCTCCAGCAGATCATGATGACATCATGGACCCAATAGCTCATTCACTGCCTTGATTCCCTT
TTGCCAACAATTTTACCAGCAGTTATACCTAACATATTATGCAATTTTCTCTTGGTGCTACC
TGATGGAATTCCTGCACTTAAAGTTCTGGCTGACTAAACAAGATATATCATTTTCTTTCTTC
TCTTTTGTGTTGGAAAATCAAGTACTTCTTTGAATGATGATCTCTTTCTTGCAAATGATATT
GTCAGTAAATAATCACGTTAGACTTCAGACCTCTGGGGATTCTTTCCGTGTCCTGAAAGAG
AATTTTAAATTATTTAATAAGAAAAAATTTATATTAATGATTGTTTCCTTTAGTAATTTAT
TGTTCTGTACTGATATTTAAATAAAGAGTTCTATTTCCCCAAAAAAAAAAAAAAAAAAAA

FIGURE 153

MAAAAATKILLCLPLLLLLSGWSRAGRADPHSLCYDITVIPKFRPGPRWCAVQGQVDEKTFL
HYDCGNKTVTPVSPLGKKLVTTAWKAQNPVLREVVDILTEQLRDIQLENYTPKEPLTLQAR
MSCEQKAEGHSSGSWQFSFDGQIFLLFDSEKRMWTTVHPGARKMKEKWENDKVVAMSFHYFS
MGDCIGWLEDFLMGMDSTLEPSAGAPLAMSSGTTQLRATATTLILCCLLIILPCFILPGI

Important features:**Signal peptide:**

amino acids 1-25

Transmembrane domain:

amino acids 224-246

N-glycosylation site.

amino acids 68-72, 82-86

N-myristoylation site.

amino acids 200-206, 210-216

Amidation site.

amino acids 77-81

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FIGURE 155

MELIPTITSWRVLILVVALTQFWCGFLCRGFHLQNHFWLLIKREFGFYSKSQYRTWQKLA
EDSTWPPINRTDYSGDGKNGFYINGGYESHEQIPKRKLKLGGQPTQHFWARL

099111 111111

GTTCTCCTTTCCGAGCCAAAATCCCAGGCGATGGTGAATTATGAACGTGCCACACC**ATGAAG**
 CTCTTGTGGCAGGTAACGTGTGCACCACCACACCTGGAATGCCATCCTGCTCCCGTTCGTCTA
 CCTCACGGCGCAAGTGTGGATTCTGTGTGCAGCCATCGCTGCTGCCGCTCAGCCGGGCCCC
 AGAACTGCCCTCCGTTTGCTCGTGCAGTAACCAGTTCAGCAAGGTGGTGTGCACGCGCCGG
 GGCCTCTCCGAGGTCCCGCAGGGTATTCCCTCGAACACCCGGTACCTCAACCTCATGGAGAA
 CAACATCCAGATGATCCAGGCCGACACCTTCCGCCACCTCCACCACCTGGAGGTCTGCAGT
 TGGGCAGGAACTCCATCCGGCAGATTGAGGTGGGGGCCTTCAACGGCCTGGCCAGCCTCAAC
 ACCCTGGAGCTGTTTCGACAACTGGCTGACAGTCATCCCTAGCGGGGCCTTTGAATACCTGTC
 CAAGCTGCGGGAGCTCTGGCTTCGCAACAACCCCATCGAAAGCATCCCCTCTTACGCCTTCA
 ACCGGGTGCCCTCCCTCATGCGCCTGGACTTGGGGGAGCTCAAGAAGCTGGAGTATATCTCT
 GAGGGAGCTTTTGAGGGGCTGTTCAACCTCAAGTATCTGAACTTGGGCATGTGCAACATTAA
 AGACATGCCCAATCTCACCCCCCTGGTGGGGCTGGAGGAGCTGGAGATGTCAGGGAACCACT
 TCCCTGAGATCAGGCCTGGCTCCTTCCATGGCCTGAGCTCCCTCAAGAAGCTCTGGGTCTATG
 AACTCACAGGTCAGCCTGATTGAGCGGAATGCTTTTGACGGGCTGGCTTCACTTGTGGAAC
 CAACTTGGCCACAATAACCTCTCTTCTTTGCCCCATGACCTCTTTACCCCGCTGAGGTACC
 TGGTGGAGTTGCATCTACACCACAACCCTTGGAACGTGTGATTGTGACATTCTGTGGCTAGCC
 TGGTGGCTTCGAGAGTATATAACCCACCAATTCCACCTGCTGTGGCCGCTGTCATGCTCCCAT
 GCACATGCGAGGCCGCTACCTCGTGGAGGTGGACCAGGCCTCCTTCCAGTGCTCTGCCCCCT
 TCATCATGGACGCACCTCGAGACCTCAACATTTCTGAGGGTCGGATGGCAGAACTTAAGTGT
 CGGACTCCCCCTATGTCTCCGTGAAGTGGTTGCTGCCCAATGGGACAGTGCTCAGCCACGC
 CTCCCCGCCACCCAAGGATCTCTGTCTCAACGACGGCACCTTGAACTTTTCCACGTGCTGC
 TTTTCAGACACTGGGGGTGTACACATGCATGGTGACCAATGTTGCAGGCAACTCCAACGCCTCG
 GCCTACCTCAATGTGAGCACGGCTGAGCTTAACACCTCCAACCTACAGCTTCTTCACCACAGT
 AACAGTGGAGACCACGGAGATCTCGCCTGAGGACACAACGCGAAAGTACAAGCCTGTTCCCTA
 CCACGTCCACTGGTTACCAGCCGGCATATAACCACCTCTACCACGGTGCTCATTCAGACTACC
 CGTGTGCCCAAGCAGGTGGCAGTACCCGCGACAGACACCACTGACAAGATGCAGACCAGCCT
 GGATGAAGTCATGAAGACCACCAAGATCATCATTGGCTGCTTTGTGGCAGTGACTCTGCTAG
 CTGCCGCCATGTTGATTGTCTTCTATAAACTTCGTAAGCGGCACCAGCAGCGGAGTACAGTC
 ACAGCCGCCCGGACTGTTGAGATAATCCAGGTGGACGAAGACATCCCAGCAGCAACATCCGC
 AGCAGCAACAGCAGCTCCGTCCGGTGTATCAGGTGAGGGGGCAGTAGTGCTGCCCACAATTC
 ATGACCATATTAACCTACAACACCTACAAACCAGCACATGGGGGCCACTGGACAGAAAACAGC
 CTGGGGAACTCTCTGCACCCACAGTCACCACTATCTCTGAACCTTATATAATTTCAGACCCA
 TACCAAGGACAAGGTACAGGAACTCAAATAT**TGA**CTCCCCCTCCCCCAAAAACTTATAAAAT
 GCAATAGAATGCACACAAAGACAGCAACTTTTGTACAGAGTGGGGAGAGACTTTTTCTTGTA
 TATGCTTATATATTAAGTCTATGGGCTGGTTAAAAAAAACAGATTATATTAATAATTAAAGA
 CAAAAAGTCAAAACA

MKLLWQVTVHHHTWNAILLFPVYLTAQVWILCAAIAAAASAGPQNCPSVCSCSNQFSKVVCT
 RRGLSEVPQGIPSNTRYLNLMENNIQMIQADTFRHLHHLEVLQLGRNSIRQIEVGAFNGLAS
 LNTLELFDNWLTVIPSGAFEYLSKLRLEWLRRNPPIESIPSYAFNRVPSLMRLDLGELKKLEY
 ISEGAFEGLFNLYLNLGMCNIKDMPNLTPLVGLLEELEMSGNHFPEIRPGSFHGLSSLLKKLW
 VMNSQVSLIERNAFDGLASLVELNLAHNNLSSSLPHDLFTPLRYLVELHLHHNPWNCDCDILW
 LAWWLREYIPTNSTCCGRCHAPMHMRGRYLVEVDQASFQCSAPFIMDAPRDLNISEGRMAEL
 KCRTPPMSSSVKLLPNGTVLSHASRHRPRISVLNDGTLNFSHVLLSDTGVYTCMVTNVAGNSN
 ASAYLNVSTAELNTSNYSFFTFTVTVETTEISPEDTTRKYKPVPTTSTGYQPAYTTSTTVLIQ
 TTRVPKQVAVPATDTTDKMQTSLDEVMKTTKIIIGCFVAVTLLAAAMLIVFYKLRRHQQRS
 TVTAARTVEIIQVDEDIPAATSAAATAAPSGVSGEGAVVLPTIHDHINYNTYKPAHGAHWTE
 NSLGNLHPTVTTISEPYIIQTHTKDKVQETQI

FIGURE 159

MELGCWTQLGLTFLQLLLISSLPREYTVINEACPGAENIMCRECCEYDQIECVCPGKREVV
GYTIPCCRNEENECDSCLIHPGCTIFENCKSCRNGSWGGLDDEFYVKGIFYCAECRAGWYGGD
CMRCGQVLRAPKGQILLESYPLNAHCEWTIHAKPGFVIQLRFVMLSLEFDYMCQYDYVEVRD
GDNRDGQIIKRVCGNERPAPIQSIGSSLHVLHFSDGSKNFDGFHAIYEEITACSSSPCFHDG
TCVLDKAGSYKCACLAGYTQRCENLLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGTV
VSFFCNSYVLSGNEKRTCQONGEWSGKQPICIKACREPKISDLVRRRVLPQVQSRETPLH
QLYSAAFQKQKLQSAPTQKPPALPFGDLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGK
WSGRAPSCIPICGKIENITAPKTQGLRWPWQAIIYRRTSGVHDGSLHKGAWFLVCSGALVNE
RTVVVAAHCVTDLGKVTMIKTADLKVVVGKFYRDDDRDEKTIQSLQISAILHPNYDPILLD
ADIAILKLLDKARISTRVQPICLAASRDLSTSFQESHITVAGWNVLADVRSFGFKNDTLRSG
VVSVDLSLLCEEQHEDHGI PVSVTDNMFCASWEPTAPSDICTAETGGIAAVSFPGRASPEPR
WHLMGLVSWSYDKTCSHRLSTAFTKVLPPKDWIERNMK

FIGURE 160

ACCAGGCATTGTATCTTCAGTTGTCATCAAGTTCGCAATCAGATTGGAAAAGCTCAACTTGA
 AGCTTTCTTGCCTGCAGTGAAGCAGAGAGATAGATATTATTACGTAATAAAAAAC**ATG**GGC
 TTCAACCTGACTTTCCACCTTTCCTACAAATTCGATTACTGTTGCTGTTGACTTTGTGCCT
 GACAGTGGTTGGGTGGGCCACCAGTAACTACTTCGTGGGTGCCATTCAAGAGATTCTTAAAG
 CAAAGGAGTTCATGGCTAATTTCCATAAGACCCTCATTTTGGGGAAGGGAAAACTCTGACT
 AATGAAGCATCCACGAAGAAGGTAGAACTTGACAACCTGTCCTTCTGTGTCTCCTTACCTCAG
 AGGCCAGAGCAAGCTCATTTTCAAACCAGATCTCACTTTGGAAGAGGTACAGGCAGAAAATC
 CCAAAGTGTCCAGAGGCCGGTATCGCCCTCAGGAATGTAAAGCTTTACAGAGGGTCGCCATC
 CTCGTTCCCCACCGAACAGAGAGAAACACCTGATGTACCTGCTGGAACATCTGCATCCCTT
 CCTGCAGAGGCAGCAGCTGGATTATGGCATCTACGTCATCCACCAGGCTGAAGGTAAAAAGT
 TTAATCGAGCCAACTCTTGAATGTGGGCTATCTAGAAGCCCTCAAGGAAGAAAATTGGGAC
 TGCTTTATATTCCACGATGTGGACCTGGTACCCGAGAATGACTTTAACCTTTACAAGTGTGA
 GGAGCATCCCAAGCATCTGGTGGTTGGCAGGAACAGCACTGGGTACAGGTTACGTTACAGTG
 GATATTTTGGGGGTGTTACTGCCCTAAGCAGAGAGCAGTTTTTCAAGGTGAATGGATTCTCT
 AACAACTACTGGGGATGGGGAGGCCGAAGACGATGACCTCAGACTCAGGGTTGAGCTCCAAAG
 AATGAAAATTTCCCGGCCCTGCCTGAAGTGGGTAAATATACAATGGTCTTCCACACTAGAG
 ACAAGGCAATGAGGTGAACGCAGAACGGATGAAGCTCTTACACCAAGTGTACGAGTCTGG
 AGAACAGATGGGTTGAGTAGTTGTTCTTATAAATTAGTATCTGTGGAACACAATCCTTTATA
 TATCAACATCACAGTGGATTTCTGGTTTGGTGCAT**TGA**CCCTGGATCTTTTGGTGATGTTTGG
 AAGAACTGATTCTTTGTTTGCAATAATTTTGGCCTAGAGACTTCAAATAGTAGCACACATTA
 AGAACCTGTTACAGCTCATTGTTGAGCTGAATTTTTCTTTTTGTATTTTCTTAGCAGAGCT
 CCTGGTGATGTAGAGTATAAAACAGTTGTAACAAGACAGCTTTCTTAGTCATTTTGATCATG
 AGGGTTAAATATTGTAATATGGATACTTGAAGGACTTTATATAAAAGGATGACTCAAAGGAT
 AAAATGAACGCTATTTGAGGACTCTGGTTGAAGGAGATTTATTTAAATTTGAAGTAATATAT
 TATGGGATAAAAGGCCACAGGAAATAAGACTGCTGAATGTCTGAGAGAACCAGAGTTGTTCT
 CGTCCAAGGTAGAAAGGTACGAAGATACAATACTGTTATTTCATTTATCCTGTACAATCATCT
 GTGAAGTGGTGGTGTGAGGTGAGAAGGCGTCCACAAAAGAGGGGAGAAAAGGCGACGAATCA
 GGACACAGTGAACCTTGGGAATGAAGAGGTAGCAGGAGGGTGGAGTGTGGCTGCAAAGGCAG
 CAGTAGCTGAGCTGGTTGCAGGTGCTGATAGCCTTCAGGGGAGGACCTGCCCAGGTATGCCT
 TCCAGTGATGCCACCAGAGAATACATTCTCTATTAGTTTTTAAAGAGTTTTTGTAAAATGA
 TTTTGTACAAGTAGGATATGAATTAGCAGTTTACAAGTTTACATATTAATAATAATAATA
 TGTCTATCAAATACCTCTGTAGTAAATGTGAAAAAGCAAAA

FIGURE 161

MGFNLT FHL SYKFRLLLLLTLCLTVVGWATSNYFVGAIQEIPKAKEFMANFHKTLILGKGKT
LTNEASTKKVELDNCPSVSPYLRGQSKLIFKPDLTLEEVQAENPKVSRGRYRPQECKALQRV
AILVPHRNREKHLMYLLEHLHPFLQRQQLDYGIYVIHQAEKGKFNRKLLNVGYLEALKEEN
WDCFIFHDVDLVPENDFNLYKCEEHPKHLVVGRNSTGYRLRYSGYFGGVTALSREQFFKVNG
FSNNYWGWGGEDDDLRLRVELQRMKISRPLPEVGKYTMVFHTRDKGNEVNAERMKLLHQVSR
VWRTDGLSSCSYKLVSVEHNPLYINITVDFWFGA

Important features:

Signal peptide:

amino acids 1-27

N-glycosylation sites:

amino acids 4-7, 220-223 and 335-338

Xylose isomerase proteins:

amino acids 191-201

CGTGGGCCCGGGGTGCGCAGCGGGCTGTGGGCGCGCCCGGAGGAGCGACCGCCGAGTTCTC
GAGCTCCAGCTGCATTCCTCCGCGTCCGCCCCACGCTTCTCCGCTCCGGGCCCCGCA**ATG**
GCCCAGGCAGTGTGGTCGCGCCTCGGCCGCATCCTCTGGCTTGCTGCCTCCTGCCCTGGGC
CCCGGCAGGGGTGGCCGCAGGCCTGTATGAACTCAATCTCACCACCGATAGCCCTGCCACCA
CGGGAGCGGTGGTGACCATCTCGGCCAGCCTGGTGGCCAAGGACAACGGCAGCCTGGCCCTG
CCCGCTGACGCCCACCTCTACCGCTTCCACTGGATCCACACCCCGCTGGTGCTTACTGGCAA
GATGGAGAAGGGTCTCAGCTCCACCATCCGTGTGGTTCGGCCACGTGCCCGGGGAATTCCCGG
TCTCTGTCTGGGTCACTGCCGCTGACTGCTGGATGTGCCAGCCTGTGGCCAGGGGCTTTGTG
GTCTTCCCCATCACAGAGTTCCTCGTGGGGGACCTTGTTGTCACCAGAACACTTCCCTACC
CTGGCCCAGCTCCTATCTCACTAAGACCGTCTGAAAGTCTCCTTCCCTCCTCCACGACCCGA
GCAACTTCCCTCAAGACCGCCTTGTTTCTCTACAGCTGGGACTTTCGGGGACGGGACCCAGATG
GTGACTGAAGACTCCGTGGTCTATTATAACTATTCCATCATCGGGACCTTCACCGTGAAGCT
CAAAGTGGTGGCGGAGTGGGAAGAGGTGGAGCCGGATGCCACGAGGGCTGTGAAGCAGAAGA
CCGGGGACTTCTCCGCCTCGCTGAAGCTGCAGGAAACCTTCGAGGCATCCAAGTGTGTTGGGG
CCCACCCTAATTACAGACCTTCCAAAAGATGACCGTGACCTTGAACCTTCCCTGGGGAGCCCTCC
TCTGACTGTGTGCTGGCGTCTCAAGCCTGAGTGCCTCCCGCTGGAGGAAGGGGAGTGCCACC
CTGTGTCCGTGGCCAGCACAGCGTACAACCTGACCCACACCTTCAGGGACCTTGGGGACTAC
TGCTTCAGCATCCGGGCCGAGAATATCATCAGCAAGACACATCAGTACCACAAGATCCAGGT
GTGGCCCTCCAGAATCCAGCCGGCTGTCTTTGCTTTCCCATGTGCTACACTTATCACTGTGA
TGTTGGCCTTCATCATGTACATGACCTGCGGAATGCCACTCAGCAAAAGGACATGGTGGAG
AACCCGGAGCCACCCTCTGGGGTCAGGTGCTGCTGCCAGATGTGCTGTGGGCCTTTCTTGCT
GGAGACTCCATCTGAGTACCTGGAAATTGTTGCTGAGAACCACGGGCTGCTCCCGCCCCCTCT
ATAAGTCTGTCAAAACTTACACCGTGT**AG**ACACTCCCCCTCCCCACCCCATCTCAGTGTTAA
CTGACTGCTGACTTGGAGTTTCCAGCAGGGTGGTGTGCACCACTGACCAGGAGGGGTTCAAT
TGCGTGGGGCTGTTGGCCTGGATCATCCATCCATCTGTACAGTTTCAGCCACTGCCACAAGCC
CCTCCCTCTCTGTACCCCTGACCCACAGCCATTACCCCATCTGTACAGTCCAGCCACTGACA
TAAGCCCCACTCGGTTACCACCCCTTGACCCCTACCTTTGAAGAGGCTTCGTGCAGGACT
TTGATGCTTGGGGTGTTCGCTGTTGACTCCTAGGTGGGCCTGGCTGCCCACTGCCCATTCCT
CTCATATTGGCACATCTGCTGTCCATTGGGGGTTCTCAGTTTCTCCCCAGACAGCCCTAC
CTGTGCCAGAGAGCTAGAAAGAAGGTCATAAAGGGTTAAAAATCCATAACTAAAGGTTGTAC
ACATAGATGGGCACACTCACAGAGAGAAGTGTGCATGTACACACACCACACACACACACACA
CACACACACACAGAAATATAAACACATGCGTCACATGGGCATTTTCAGATGATCAGCTCTGTA
TCTGGTTAAGTCGGTTGCTGGGATGCACCCTGCACTAGAGCTGAAAGGAAATTTGACCTCCA
AGCAGCCCTGACAGGTTCTGGGCCCGGGCCCTCCCTTTGTGCTTTGTCTCTGCAGTTCTTGC
GCCCTTTATAAGGCCATCCTAGTCCCTGCTGGCTGGCAGGGGCCTGGATGGGGGGCAGGACT
AATACTGAGTGATTGCAGAGTGCTTTATAAATATCACCTTATTTTATCGAAACCCATCTGTG
AAACTTTCACTGAGGAAAAGGCCTTGCAGCGGTAGAAGAGGTTGAGTCAAGGCCGGGCGCGG
TGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGGTGGATCACGAGATCAGGA
GATCGAGACCACCCTGGCTAACACGGTGAAACCCCGTCTCTACTAAAAAATACAAAAGTT
AGCCGGGCGTGGTGGTGGGTGCCTGTAGTCCAGCTACTCGGGAGGCTGAGGCAGGAGAATG
GTGCGAACCCGGGAGGCGGAGCTTGCAGTGAGCCAGATGGCGCCACTGCACTCCAGCCTGA
GTGACAGAGCGAGACTCTGTCTCCA

FIGURE 163

MAQAVWSRLGRILWLACLLPWAPAGVAAGLYELNLTTDSPATTGAVVTISASLVAKDNGSLA
LPADAHLYRFHWIHTPLVLTGKMEKGLSSTIRVVGHVPGEFPVSVWVTAADCWMCQPVARGF
VVLPITEFLVGDLVVTQNTSLPWSSYLTKTVLKVSFLLHDPSNFLKTALFLYSWDFGDGTQ
MVTEDSVVYYNYSIIGTFTVKLKVVAEWEEVEPDATRAVKQKTGDFSASLKLQETLRGIQVL
GPTLIQTFQKMTVTNLNFLGSPPLTVCWRLKPECLPLEEGECHPVSVASTAYNLTHTRDPGD
YCFSIRAENIISKTHQYHKIQVWPSRIQPAVFAFPCATLITVMLAFIMYMTLRNATQQKDMV
ENPEPPSGVRCCCQMCCGPFLLETPSEYLEIVRENHGLLPPLYKSVKTYTV

Important features of the protein:**Signal peptide:**

amino acids 1-24

Transmembrane domain:

amino acids 339-362

N-glycosylation sites.

amino acids 34-37, 58-61, 142-145, 197-200, 300-303 and 364-367

FIGURE 164

GCTCAAGACCCAGCAGTGGGACAGCCAGACAGACGGCACG**ATG**GCACTGAGCTCCCAGATCT
GGGCCGCTTGCCTCCTGCTCCTCCTCCTCGCCAGCCTGACCAGTGGCTCTGTTTTCCCA
CAACAGACGGGACAACCTTGCAGAGCTGCAACCCCAGGACAGAGCTGGAGCCAGGGCCAGCTG
GATGCCCATGTTCCAGAGGCGAAGGAGGCGAGACACCCACTTCCCCATCTGCATTTTCTGCT
GCGGCTGCTGTCATCGATCAAAGTGTGGGATGTGCTGCAAGACG**TAG**AACCTACCTGCCCTG
CCCCCGTCCCCTCCCTTCTTTATTTATTCCTGCTGCCCCAGAACATAGGTCTTGGAATAAAA
TGGCTGGTTCTTTTGTTCCTTCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAA

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FIGURE 165

MALSSQIWAACLLLLLLLLASLTSGSVFPQQTGQLAELQPQDRAGARASWMPMFQRRRRRDTH
FPICIFCCGCCHRSKCGMCCKT

FIGURE 166

CTGTCAGGAAGGACCATCTGAAGGCTGCAATTTGTTCTTAGGGAGGCAGGTGCTGGCCTGGC
 CTGGATCTTCCACC**ATG**TTTCTGTTGCTGCCTTTTGATAGCCTGATTGTCAACCTTCTGGGC
 ATCTCCCTGACTGTCCTCTTACCCTCCTTCTCGTTTTTCATCATAGTGCCAGCCATTTTTGG
 AGTCTCCTTTGGTATCCGCAAACCTCTACATGAAAAGTCTGTTAAAAATCTTTGCGTGGGCTA
 CCTTGAGAATGGAGCGAGGAGCCAAGGAGAAGAACCACCAGCTTTACAAGCCCTACACCAAC
 GGAATCATTGCAAAGGATCCCACTTCACTAGAAGAAGAGATCAAAGAGATTCTGTCGAAGTGG
 TAGTAGTAAGGCTCTGGACAACACTCCAGAGTTCGAGCTCTCTGACATTTTCTACTTTTGCC
 GGAAAGGAATGGAGACCATTATGGATGATGAGGTGACAAAGAGATTCTCAGCAGAAGAAGT
 GAGTCCTGGAACCTGCTGAGCAGAACCAATTATAACTTCCAGTACATCAGCCTTCGGCTCAC
 GGTCTGTGGGGGTTAGGAGTGCTGATTCGGTACTGCTTTCTGCTGCCGCTCAGGATAGCAC
 TGGCTTTCACAGGGATTAGCCTTCTGGTGGTGGGCACAACCTGTGGTGGGATACTTGCCAAAT
 GGGAGGTTTAAGGAATTCATGAGTAAACATGTTCACTTAATGTGTTACCGGATCTGCGTGCG
 AGCGCTGACAGCCATCATCACCTACCATGACAGGGAAAACAGACCAAGAAATGGTGGCATCT
 GTGTGGCCAATCATACCTCACCGATCGATGTGATCATCTTGGCCAGCGATGGCTATTATGCC
 ATGGTGGGTCAAGTGCACGGGGGACTCATGGGTGTGATTGAGAGAGCCATGGTGAAGGCCTG
 CCCACACGCTCTGGTTTGAGCGCTCGGAAGTGAAGGATCGCCACCTGGTGGCTAAGAGACTGA
 CTGAACATGTGCAAGATAAAAGCAAGCTGCCTATCCTCATCTTCCCAGAAGGAACCTGCATC
 AATAATACATCGGTGATGATGTTCAAAAAGGGAAGTTTTGAAATTGGAGCCACAGTTTACCC
 TGTGCTATCAAGTATGACCCTCAATTTGGCGATGCCTTCTGGAACAGCAGCAAATACGGGA
 TGGTGACGTACCTGCTGCGAATGATGACCAGCTGGGCCATTGTCTGCAGCGTGTGGTACCTG
 CCTCCCATGACTAGAGAGGCAGATGAAGATGCTGTCCAGTTTGCGAATAGGGTGAATCTGC
 CATTGCCAGGCAGGGAGGACTTGTGGACCTGCTGTGGGATGGGGGCCTGAAGAGGGAGAAGG
 TGAAGGACACGTTCAAGGAGGAGCAGCAGAAGCTGTACAGCAAGATGATCGTGGGGAACCA
 AAGGACAGGAGCCGCTCC**TGA**GCCTGCCTCCAGCTGGCTGGGGCCACCGTGCGGGGTGCCAA
 CGGGCTCAGAGCTGGAGTTGCCGCCGCCGCCCCCACTGCTGTGTCTTTCCAGACTCCAGGG
 CTCCCCGGGCTGCTCTGGATCCCAGGACTCCGGCTTTCGCCGAGCCGCAGCGGGATCCCTGT
 GCACCCGGCGCAGCCTACCTTGGTGGTCTAAACGGATGCTGCTGGGTGTTGCGACCCAGGA
 CGAGATGCCTTGTTTTCTTTTACAATAAGTCGTTGGAGGAATGCCATTAAAGTGAATCCCCA
 CCTTTGCACGCTGTGCGGGCTGAGTGGTTGGGGAGATGTGGCCATGGTCTTGTGCTAGAGAT
 GGCGGTACAAGAGTCTGTTATGCAAGCCCGTGTGCCAGGGATGTGCTGGGGGCGGCCACCCG
 CTCTCCAGGAAAGGCACAGCTGAGGCACTGTGGCTGGCTTCGGCCTCAACATCGCCCCCAGC
 CTTGGAGCTCTGCAGACATGATAGGAAGGAACTGTCATCTGCAGGGGCTTTCAGCAAAATG
 AAGGGTTAGATTTTTATGCTGCTGCTGATGGGGTTACTAAAGGGAGGGGAAGAGGCCAGGTG
 GGCCGCTGACTGGGCCATGGGGAGAACGTGTGTTTCGTACTCCAGGCTAACCCCTGAACTCCCC
 ATGTGATGCGCGCTTTGTTGAATGTGTGTCTCGTTTTCCCATCTGTAATATGAGTCGGGGG
 GAATGGTGGTGATTCCCTACCTCACAGGGCTGTTGTGGGGATTAAAGTGCTGCGGGTGAGTGA
 AGGACACATCACGTTCAAGTACAGGCCACAAAACGGGGCACGGCAGGCCTGAG
 CTCAGAGCTGCTGCACTGGGCTTTGGATTTGTTCTTGTGAGTAAATAAACTGGCTGGTGAA
 TGA

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FIGURE 167

MFLLLPFDSLIVNLLGISLTVLFTLLLVFIIVPAIFGVSFGIRKLYMKSLLKIFAWATLRME
RGAKEKNHQLYKPYTNGIIAKDPTSLEEEIKEIRRS GSSKALDNTPEFELSDIFYFCRKGME
TIMDDEVTKRFSAAEELESWNLLSRTNYNFQYISLRLTVLWGLGVLI RYCFLLPLRIAL AFTG
ISLLVVGTTTVGYLPNGRFKEEFMSKHVHLMCYRICVRALTAIITYHDREN RPRNGGICVANH
TSPIDV IILASDGY YAMVGQVHGGLMGVIQ RAMVKACPHVWFERSEVKDRHLVAKRLTEHVQ
DKSKLPILIFPEGTCINNTSVMMFKKGSFEIGATVYPVAIKYDPQFGDAFWNSSKYGMV TYL
LRMMTSWAI VCSVWYLP PMTREADED AVQFANRVKSAIARQGGLVDLLWDGGLKREKV KDTF
KEEQQKLYSKMIVGNHKDRSRS

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FIGURE 168

GCCCCTCGAAACCAGGACTCCAGCACCTCTGGTCCCGCCCTCACCCGGACCCCTGGCCCTCA
CGTCTCCTCCAGGG**ATG**CGCTGGCGGCTTTGATGATCGCCCTCGGCAGCCTCGGCCTCCAC
ACCTGGCAGGCCCAGGCTGTTCCCAACATCCTGCCCCTGGGCCTGGCTCCAGACACCTTTGA
CGATACCTATGTGGGTTGTGCAGAGGAGATGGAGGAGAAGGCAGCCCCCTGCTAAAGGAGG
AAATGGCCCAACCATGCCCTGCTGCGGGAATCCTGGGAGGCAGCCAGGAGACCTGGGAGGAC
AAGCGTCGAGGGCTTACCTTGCCCCCTGGCTTCAAAGCCCAGAATGGAATAGCCATTATGGT
CTACACCAACTCATCGAACACCTTGTACTGGGAGTTGAATCAGGCCGTGCGGACGGGCGGAG
GCTCCCGGGAGCTCTACATGAGGCACTTTCCTTCAAGGCCCTGCATTTCTACCTGATCCGG
GCCCTGCAGCTGCTGCGAGGCAGTGGGGGCTGCAGCAGGGGACCTGGGGAGGTGGTGTTCG
AGGTGTGGGCAGCCTTCGCTTTGAACCCAAGAGGCTGGGGGACTCTGTCCGCTTGGGCCAGT
TTGCCTCCAGCTCCCTGGATAAGGCAGTGGCCACAGATTTGGGGAGAAGAGGCGGGGCTGT
GTGTCTGCGCCAGGGGTGCAGCTAGGGTCACAATCTGAGGGGGCCTCCTCTCTGCCCCCTG
GAAGACTCTGCTCTTGCCCCCTGGAGAGTTCCAGCTCTCAGGGGTTGGGCCC**TGA**AAGTCCA
ACATCTGCCACTTAGGAGCCCTGGGAACGGGTGACCTTCATATGACGAAGAGGCACCTCCAG
CAGCCTTGAGAAGCAAGAACATGGTTCCGGACCCAGCCCTAGCAGCCTTCTCCCCAACCAGG
ATGTTGGCCTGGGGAGGCCACAGCAGGGCTGAGGGAACTCTGCTATGTGATGGGGACTTCCT
GGGACAAGCAAGGAAAGTACTGAGGCAGCCACTTGATTGAACGGTGTGCAATGTGGAGACA
TGGAGTTTTATTGAGGTAGCTACGTGATTAAATGGTATTGCAGTGTGGA

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FIGURE 169

MALAALMIALGSLGLHTWQAQAVPTILPLGLAPDTFDDTYVGCAEEMEEKAAPLLKEEMAHH
ALLRESWEAAQETWEDKRRGLTLPPGFKAQNGIAIMVYTNSSNTLYWELNQAVRTGGGSREL
YMRHFPPKALHFYLIRALQLLRGSGGCSRGPGEVVFRGVGSLRFEPKRLGDSVRLGQFASSS
LDKAVAHRFGEKRRGCVSAPGVQLGSQSEGASSLPPWKTLLLAPGEFQLSGVGP

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FIGURE 170

GTGGCTTTCATTTTCAGTGGCTGACTTCCAGAGAGCAATATGGCTGGTTCCCCAACATGCCTCA
CCCTCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCCTCTGGACCCGTGAAAGAGCTG
GTCGGTTCCGTTGGTGGGGCCGTGACTTTCCCCCTGAAGTCCAAAGTAAAGCAAGTTGACTC
TATTGTCTGGACCTTCAACACAACCCCTCTTGTCAACATACAGCCAGAAGGGGGCACTATCA
TAGTGACCCAAAATCGTAATAGGGAGAGAGTAGACTTCCCAGATGGAGGCTACTCCCTGAAG
CTCAGCAAACCTGAAGAAGAATGACTCAGGGATCTACTATGTGGGGATATACAGCTCATCACT
CCAGCAGCCCTCCACCCAGGAGTACGTGCTGCATGTCTACGAGCACCTGTCAAAGCCTAAAG
TCACCATGGGTCTGCAGAGCAATAAGAATGGCACCTGTGTGACCAATCTGACATGCTGCATG
GAACATGGGGAAGAGGATGTGATTTATACCTGGAAGGCCCTGGGGCAAGCAGCCAATGAGTC
CCATAATGGGTCCATCCTCCCCATCTCCTGGAGATGGGGAGAAAGTGATATGACCTTCATCT
GCGTTGCCAGGAACCCTGTCAGCAGAAACTTCTCAAGCCCCATCCTTGCCAGGAAGCTCTGT
GAAGGTGCTGCTGATGACCCAGATTCTCTCCATGGTCCTCCTGTGTCTCCTGTTGGTGCCCT
CCTGCTCAGTCTCTTTGTACTGGGGCTATTTCTTTGGTTTCTGAAGAGAGAGAGACAAGAAG
AGTACATTGAAGAGAAGAAGAGAGTGGACATTTGTCTGGGAAACTCCTAACATATGCCCCCAT
TCTGGAGAGAACACAGAGTACGACACAATCCCTCACACTAATAGAACAATCCTAAAGGAAGA
TCCAGCAAATACGGTTTACTCCACTGTGGAAATACCGAAAAAGATGGAAAATCCCCACTCAC
TGCTCACGATGCCAGACACACCAAGGCTATTTGCCTATGAGAATGTTATCTAGACAGCAGTG
CACTCCCCTAAGTCTCTGCTCA

MAGSPTCLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPLVT
IQPEGGTIIVTVQNRNRERVDFFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEYVLHV
YEHLSPKPVMTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSILPISWRW
GESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLCLLLVPLLLSLFVLGLFLW
FLKRERQEEYIEKKRVDICRETPNICPHSGENTYDTIPHTNRTILKEDPANTVYSTVEIP
KKMENPHSLLTMPDTPRLFAYENVI

FIGURE 172

CTGGTTCCCCAACATGCCTCACCCCTCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCC
TCTGGACCCCGTGAAAGAGCTGGTCGGTTCCGTTGGTGGGGCCGTGACTTTCCCCCTGAAGTC
CAAAGTAAAGCAAGTTGACTCTATTGTCTGGACCTTCAACACAACCCCTCTTGTCACCATAC
AGCCAGAAGGGGGCCTATCATAGTGACCCAAAATCGTAATAGGGAGAGAGTAGACTTCCCA
GATGGAGGCTACTCCCTGAAGCTCAGCAAACCTGAAGAAGAATGACTCAGGGATCTACTATGT
GGGGATATACAGCTCATCACTCCAGCAGCCCTCCACCCAGGAGTACGTGCTGCATGTCTACG
AGCACCTGTCAAAGCCTAAAGTCACCATGGGTCTGCAGAGCAATAAGAATGGCACCTGTGTG
ACCAATCTGACATGCTGCATGGAACATGGGGAAGAGGATGTGATTTATACCTGGAAGGCCCT
GGGGCAAGCAGCCAATGAGTCCCATAATGGGTCCATCCTCCCCATCTCCTGGAGATGGGGAG
AAAGTGATATGACCTTCATCTGCGTTGCCAGGAACCCCTGTCAGCAGAACTTCTCAAGCCCC
ATCCTTGCCAGGAAGCTCTGTGAAGGTGCTGCTGATGACCCAGATTCTCCATGGTCCTCCT
GTGTCTCCTGTTGGTGCCCCCTCTGCTCAGTCTCTTTGTACTGGGGCTATTTCTTTGGTTTC
TGAAGAGAGAGAGACAAGAAGAGTACATTGAAGAGAAGAAGAGAGTGACATTTGTCTGGGAA
ACTCCTAACATATGCCCCCATTTCTGGAGAGAACACAGAGTACGACACAATCCCTCACACTAA
TAGAACAATCCTAAAGGAAGATCCAGCAAATACGGTTTACTCCACTGTGGAAATACCGAAAA
AGATGGAAAATCCCCACTCACTGCTCACGATGCCAGACACACCAAGGCTATTTGCCTATGAG
AATGTTATCTAGACAGCAGTGCCTCCCTAAGTCTCTGCTCAAAAAAAAAAAAAAAAAAAAAA

FIGURE 173

GAAAGACGTGGTCCTGACAGACAGACAATCCTATTCCCTACCAAA**ATGA**AAGATGCTGCTGCT
GCTGTGTTTGGGACTGACCCTAGTCTGTGTCCATGCAGAAGAAGCTAGTTCTACGGGAAGGA
ACTTTAATGTAGAAAAGATTAAATGGGGAATGGCATACTATTATCCTGGCCTCTGACAAAAGA
GAAAAGATAGAAGAACATGGCAACTTTAGACTTTTTCTGGAGCAAATCCATGTCTTGGAGAA
TTCCTTAGTTCTTAAAGTCCATACTGTAAGAGATGAAGAGTGCTCCGAATTATCTATGGTTG
CTGACAAAACAGAAAAGGCTGGTGAATATTCTGTGACGTATGATGGATTCAATACATTTACT
ATACCTAAGACAGACTATGATAACTTTCTTATGGCTCACCTCATTAACGAAAAGGATGGGGA
AACCTTCCAGCTGATGGGGCTCTATGGCCGAGAACCAGATTTGAGTTCAGACATCAAGGAAA
GGTTTGCACAACATATGTGAGGAGCATGGAATCCTTAGAGAAAATATCATTGACCTATCCAAT
GCCAATCGCTGCCTCCAGGCCCGAGAATGAAGAATGGCCTGAGCCTCCAGTGTTGAGTGGAC
ACTTCTCACCAGGACTCCACCATCATCCCTTCCTATCCATACAGCATCCCCAGTATAAATTC
TGTGATCTGCATTCCATCCTGTCTCACTGAGAAGTCCAATTCCAGTCTATCAACATGTTACC
TAGGATACCTCATCAAGAATCAAAGACTTCTTTAAATTTCTCTTTGATACACCCTTGACAAT
TTTTCATGAAATTATTCCTCTTCCTGTTCAATAAATGATTACCCTTGCACTTAA

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FIGURE 174

MKMLLLLCLGLTLVCVHAAEEASSTGRNFNVEKINGEWHTIILASDKREKIEEHGNFRLFLEQ
IHVLENSLVLKVHTVRDEECSELSMVADKTEKAGEYSVTYDGFNTFTIPKTDYDNFLMAHLI
NEKDGETFQLMGLYGREPDLSSDIKERFAQLCEEHGILRENIIDLSNANRCLQARE

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FIGURE 175

GGCTCGAGCGTTTCTGAGCCAGGGGTGACC**ATG**ACCTGCTGCGAAGGATGGACATCCTGCAA
TGGATTCAGCCTGCTGGTTCTACTGCTGTTAGGAGTAGTTCTCAATGCGATACCTCTAATTG
TCAGCTTAGTTGAGGAAGACCAATTTTCTCAAACCCCATCTCTTGCTTTGAGTGGTGGTTC
CCAGGAATTATAGGAGCAGGTCTGATGGCCATTCCAGCAACAACAATGTCCTTGACAGCAAG
AAAAAGAGCGTGCTGCAACAACAGAACTGGAATGTTTCTTTCATCATTTTTTCAGTGTGATCA
CAGTCATTGGTGCTCTGTATTGCATGCTGATATCCATCCAGGCTCTCTTAAAAGGTCCTCTC
ATGTGTAATTCTCCAAGCAACAGTAATGCCAATTGTGAATTTTCATTGAAAAACATCAGTGA
CATTCATCCAGAATCCTTCAACTTGCAGTGGTTTTTCAATGACTCTTGTGCACCTCCTACTG
GTTTCAATAAACCCACCAGTAACGACACCATGGCGAGTGGCTGGAGAGCATCTAGTTTCCAC
TTCGATTCTGAAGAAAACAAACATAGGCTTATCCACTTCTCAGTATTTTTAGGTCTATTGCT
TGTTGGAATTCTGGAGGTCCTGTTTGGGCTCAGTCAGATAGTCATCGGTTTCCTTGGCTGTC
TGTGTGGAGTCTCTAAGCGAAGAAGTCAAATTGTG**TAG**TTTAATGGGAATAAAATGTAAGTA
TCAGTAGTTTGAAAAAAAAAAAA

TGTGTGGAGTCTCTAAGCGAAGAAGTCAAATTGTG**TAG**TTTAATGGGAATAAAATGTAAGTA

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FIGURE 176

MTCCEGWTSCNGFSLLVLLLLGVVLNAIPLIVSLVEEDQFSQNPISCFEWWFPGIIGAGLMA
IPATTMSLTARKRACCNRTGMFLSSFFSVITVIGALYCM LISIQALLKGPLMCNSPSNSNA
NCEFSLKNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMASGWRASSFHFDSEENKHRL
IHFSVFLGLLLVGILEVLFGLSQIVIGFLGCLCGVSKRRSQIV

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FIGURE 177

GTCGAATCCAAATCACTCATTGTGAAAGCTGAGCTCACAGCCGAATAAGCCACC**ATG**AGGCT
GTCAGTGTGTCTCCTGATGGTCTCGCTGGCCCTTTGCTGCTACCAGGCCCATGCTCTTGTCT
GCCCAGCTGTTGCTTCTGAGATCACAGTCTTCTTATTCTTAAGTGACGCTGCGGTAAACCTC
CAAGTTGCCAAACTTAATCCACCTCCAGAAGCTCTTGCAGCCAAGTTGGAAGTGAAGCACTG
CACCGATCAGATATCTTTTAAGAAACGACTCTCATTGAAAAAGTCCTGGTGGAA**TAG**TGAA
AAAATGTGGTGTGTGACATGTAAAAATGCTCAACCTGGTTTCCAAAGTCTTTCACGACACC
CTGATCTTCACTAAAAATTGTAAAGGTTCAACACGTTGCTTTAATAAATCACTTGCCCTGC

TGGTGTGTGACATGTAAAAATGCTCAACCTGGTTTCCAAAGTCTTTCACGACACC

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FIGURE 178

MRLSVCLLMVSLALCCYQAHALVCPAVASEITVFLFLSDAAVNLQVAKLNPPPEALAAKLEV
KHCTDQISFKKRLSLKKSWWK

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FIGURE 179

ATCCGTTCTCTGCGCTGCCAGCTCAGGTGAGCCCTCGCCAAGGTGACCTCGCAGGACACTGG
TGAAGGAGCAGTGAGGAACCTGCAGAGTCACACAGTTGCTGACCAATTGAGCTGTGAGCCTG
GAGCAGATCCGTGGGCTGCAGACCCCCGCCCCAGTGCCTCTCCCCCTGCAGCCCTGCCCCCTC
GAACTGTGAC**ATG**GAGAGAGTGACCCTGGCCCTTCTCCTACTGGCAGGCCTGACTGCCTTGG
AAGCCAATGACCCATTTGCCAATAAAGACGATCCCTTCTACTATGACTGGAAAAACCTGCAG
CTGAGCGGACTGATCTGCGGAGGGCTCCTGGCCATTGCTGGGATCGCGGCAGTTCTGAGTGG
CAAATGCAAATACAAGAGCAGCCAGAAGCAGCACAGTCCTGTACCTGAGAAGGCCATCCCAC
TCATCACTCCAGGCTCTGCCACTACTTGCT**TGA**GCACAGGACTGGCCTCCAGGGATGGCCTGA
AGCCTAACACTGGCCCCCAGCACCTCCTCCCCTGGGAGGCCTTATCCTCAAGGAAGGACTTC
TCTCCAAGGGCAGGCTGTTAGGCCCTTTCTGATCAGGAGGCTTCTTTATGAATTAAACTCG
CCCCACCACCCCTCA

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FIGURE 180

MERVTLALLLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSGKCK
YKSSQKQHSPVPEKAIPLITPGSATTC

1. 2. 3. 4. 5. 6. 7. 8. 9. 10. 11. 12. 13. 14. 15. 16. 17. 18. 19. 20. 21. 22. 23. 24. 25. 26. 27. 28. 29. 30. 31. 32. 33. 34. 35. 36. 37. 38. 39. 40. 41. 42. 43. 44. 45. 46. 47. 48. 49. 50. 51. 52. 53. 54. 55. 56. 57. 58. 59. 60. 61. 62. 63. 64. 65. 66. 67. 68. 69. 70. 71. 72. 73. 74. 75. 76. 77. 78. 79. 80. 81. 82. 83. 84. 85. 86. 87. 88. 89. 90. 91. 92. 93. 94. 95. 96. 97. 98. 99. 100.

FIGURE 181

GGAGAAGAGGTTGTGTGGGACAAGCTGCTCCCGACAGAAGG**ATG**TCGCTGCTGAGCCTGCCC
TGGCTGGGCCTCAGACCGGTGGCAATGTCCCCATGGCTACTCCTGCTGCTGGTTGTGGGCTC
CTGGCTACTCGCCCGCATCCTGGCTTGGACCTATGCCTTCTATAACAACTGCCGCCGGCTCC
AGTGTTTCCCACAGCCCCCAAACGGAACTGGTTTTGGGGTCACCTGGGCCTGATCACTCCT
ACAGAGGAGGGCTTGAAGGACTCGACCCAGATGTGGGCCACCTATTCCCAGGGCTTTACGGT
ATGGCTGGGTCCCATCATCCCCCTTCATCGTTTTATGCCACCCTGACACCATCCGGTCTATCA
CCAATGCCTCAGCTGCCATTGCACCCAAGGATAATCTCTTCATCAGGTTCTGAAGCCCTGG
CTGGGAGAAGGGATACTGCTGAGTGGCGGTGACAAGTGGAGCCGCCACCGTCGGATGCTGAC
GCCCCGCTTCCATTTCAACATCCTGAAGTCCTATATAACGATCTTCAACAAGAGTGCAAACA
TCATGCTTGACAAGTGGCAGCACCTGGCCTCAGAGGGCAGCAGTCGTCTGGACATGTTTGAG
CACATCAGCCTCATGACCTTGGACAGTCTACAGAAATGCATCTTCAGCTTTGACAGCCATTG
TCAGGAGAGGCCCAGTGAATATATTGCCACCATCTTGGAGCTCAGTGCCCTTGTAGAGAAAA
GAAGCCAGCATATCCTCCAGCACATGGACTTTCTGTATTACCTCTCCCATGACGGGCGGCGC
TTCCACAGGGCCTGCCGCCTGGTGCATGACTTCACAGACGCTGTCATCCGGGAGCGGCGTCTG
CACCTCCCCACTCAGGGTATTGATGATTTTTTCAAAGACAAAGCCAAGTCCAAGACTTTGG
ATTTCAATTGATGTGCTTCTGCTGAGCAAGGATGAAGATGGGAAGGCATTGTCAGATGAGGAT
ATAAGAGCAGAGGCTGACACCTTCATGTTTGGAGGCCATGACACCACGGCCAGTGGCCTCTC
CTGGGTCTGTACAACCTTGCGAGGCACCCAGAATACCAGGAGCGCTGCCGACAGGAGGTGC
AAGAGCTTCTGAAGGACCGCGATCCTAAAGAGATTGAATGGGACGACCTGGCCCAGCTGCCC
TTCTTGACCATGTGCGTGAAGGAGAGCCTGAGGTTACATCCCCCAGCTCCCTTCATCTCCCG
ATGCTGCACCCAGGACATTGTTCTCCAGATGGCCGAGTCATCCCCAAAGGCATTACCTGCC
TCATCGATATTATAGGGGTCCATCACAACCCAACTGTGTGGCCGGATCCTGAGGTCTACGAC
CCCTTCCGCTTTGACCCAGAGAACAGCAAGGGGAGGTCACCTCTGGCTTTTATTCTTTCTC
CGCAGGGCCCAGGAACTGCATCGGGCAGGCGTTCGCCATGGCGGAGATGAAAGTGGTCCTGG
CGTTGATGCTGCTGCACTTCGGTTCTGCGAGACCACACTGAGCCCCGAGGAAGCTGGAA
TTGATCATGCGCGCCGAGGGCGGGCTTTGGCTGCGGGTGGAGCCCCTGAATGTAGGCTTGCA
GTGACTTTCTGACCCATCCACCTGTTTTTTTGCAGATTGTCATGAATAAAACGGTGCTGTCAA

FIGURE 182

MSLLSLPWLGLRPVAMSPWLLLLLVVGSWLLARILAWTYAFYNNCRRLQCFPQPPKRNWFWG
HLGLITPTEEGLKDSTQMSATYSQGFTVWLGPIIPFIVLCHPDTIRSITNASAAIAPKDNLF
IRFLKPWLGE GILLSGGDKWSRHRRLTPAFHFNILKSYITIFNKSANIMLDKWQHLASEGS
SRLDMFEHISLMTLDSLQKCIFSFDSHCQERPSEYIATILELSALVEKRSQHILQHMDFLYY
LSHDGRRFHRACRLVHDFTDVIRERRRTLPTQGIDDFKDKAKSKTLDFIDVLLLSKDEDG
KALSDEDIRAEADTFMFGGHDTTASGLSWVLYNLARHPEYQERCRQEVQELLKDRDPKEIEW
DDLAQLPFLTMCVKESLRLHPPAPFISRCCTQDIVLPDGRVIPKGITCLIDIIGVHHNPTVW
PDPEVYDPFRFDPENSKGRSPLAFIPFSAGPRNCIGQAFAMAEMKVVLALMLLHFRFLPDHT
EPRRKLELIMRAEGGLWLRVEPLNVGLQ

CAACAGAAGCCAAGAAGGAAGCCGTCTATCTTGTGGCGATC**ATG**TATAAGCTGGCCTCCTGC
TGTTTGCTTTTCACAGGATTCTTAAATCCTCTCTTATCTCTTCCTCTCCTTGACTCCAGGGA
AATATCCTTTCAACTCTCAGCACCTCATGAAGACGCGCGCTTAACTCCGGAGGAGCTAGAAA
GAGCTTCCCTTCTACAGATATTGCCAGAGATGCTGGGTGCAGAAAGAGGGGATATTCTCAGG
AAAGCAGACTCAAGTACCAACATTTTTTAACCCAAGAGGAAATTTGAGAAAGTTTCAGGATTT
CTCTGGACAAGATCCTAACATTTTACTGAGTCATCTTTTGGCCAGAATCTGGAAACCATACA
AGAAACGTGAGACTCCTGATTGCTTCTGGAAATACTGTGTC**TGA**AGTGAAATAAGCATCTGT
TAGTCAGCTCAGAAACACCCATCTTAGAATATGAAAAATAACACAATGCTTGATTTGAAAC
AGTGTGGAGAAAACTAGGCAAACCTACACCCTGTTCAATTGTTACCTGGAAAATAAATCCTCT
ATGTTTTGCACAAAAAAAAAAAAAAAAA

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FIGURE 184

MYKLASCCLLFTGFLNPLLSLPLLDREISFQLSAPHEDARLTPEELERASLLQILPEMLGA
ERGDILRKADSSTNIFNPRGNLRKFQDFSGQDPNILLSHLLARIWKPYKKRETPDCFWKYCV

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FIGURE 185

GAACATTTTTAGTTCCCAAGGAATGTACATCAGCCCCACGGAAGCTAGGCCACCTCTGGGAT
GGGGTTGCTGGTTTAAAACAAACGCCAGTCATCCTATATAAGGACCTGACAGCCACCAGGCA
CCACCTCCGCCAGGAAGTGCAGGCCCCACCTGTCTGCAACCCAGCTGAGGCC**ATG**CCCTCCCC
AGGGACCGTCTGCAGCCTCCTGCTCCTCGGCATGCTCTGGCTGGACTTGGCCATGGCAGGCT
CCAGCTTCCTGAGCCCTGAACACCAGAGAGTCCAGCAGAGAAAGGAGTCGAAGAAGCCACCA
GCCAAGCTGCAGCCCCGAGCTCTAGCAGGCTGGCTCCGCCCCGGAAGATGGAGGTCAAGCAGA
AGGGGCAGAGGATGAACTGGAAGTCCGGTTCAACGCCCCCTTTGATGTTGGAATCAAGCTGT
CAGGGGTTTCAGTACCAGCAGCACAGCCAGGCCCTGGGGAAGTTTCTTCAGGACATCCTCTGG
GAAGAGGCCAAAGAGGCCCCAGCCGACAAG**TGA**TCGCCACAAGCCTTACTCACCTCTCTCT
AAGTTTAGAAGCGCTCATCTGGCTTTTCGCTTGCTTCTGCAGCAACTCCCACGACTGTTGTA
CAAGCTCAGGAGGCGAATAAATGTTCAAAGTGT

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FIGURE 186

MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKPPAKLQPRALAGWLRPEDG
GQAEGAEDELEVRFNAPFDVGIKLSGVQYQQHSQALGKFLQDILWEEAKEAPADKO

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FIGURE 187

CGGCCACAGCTGGCATGCTCTGCCTGATCGCCATCCTGCTGTATGTCCTCGTCCAGTACCTC
GTGAACCCCGGGGTGCTCCGCACGGACCCAGATGTCAAGAATATGAACACGTGGCTGCTGT
TCCTCCCCCTGTTCCCGGTGCAGGTGCAGACCCTGATAGTCGTGATCATCGGGATGCTCGTG
CTCCTGCTGGACTTTCTTGGCTTGGTGCACCTGGGCCAGCTGCTCATCTTCCACATCTACCT
GAGTATGTCCCCACCCTAAGCCCCGATCCCCCAAGGCTGGGTGGTCAGAGCTGCTCATC
TTACACCTCTACTTGAGTATGTCCCTAACCTGAGCCCCCACGCCTGGGGCCAGAGTCTTT
GTCCCCCGTGTGCGCATGTGTTCAAGGTCAGCCTCTCCAGAAGTGAGATCATGGACAAAAA
GGGCAAATCACAGGAAGAAATTAAATCCATGAGGACCCAGCAGGCCAGCAAGAAGCTGAAC
TCACGCCGAGACCTGCAGGAGTGGTGCCAGGTGCTTGAAGTAACAAGTTTAAATGTTTCA
GACAATGGAATGGAATCTATTAGGCAAGAACAGGACATTATGAAATAAGGACAGGTGGACTT
CCAAAAACACAAGTAGAAATTCTAACAAATGAAATATATTACAGGCAGGTCACCCCTAACCA
AACAACTGAAGCGAGAGCTGTGGTCTTGCTTGGTCTCACAGTGGGCACAGCGGTAGGCGGTC
AGTCATGTTGCTGAACGACGGAGGGTAAACTCCCCAGCCCCAAGAAAACCTGTGTTGGAAGT
AACAAACACCTCCCTGCTCCTGGCACCAGCCGTTTTTGGTCATGGTGGGCCAGCTGCAAAGCG
TCTTCCATTCTCTGGGCAGTGGTGGCCCCGAGGCTGTGGCCTCTCAGGGGGTTTCTGTGGAC
ACGGGCAGCAGAGTGTGTCCAGGCCAGCCCCAAGAATGCCCTGCTCCTGACAGCTTGGCCA
ACCCCTGGTCAGGGCAGAGGGAGTTGGGTGGGTCAGGCTCTGGGCTCACCTCCATCTCCAGA
GCATCCCCCTGCCTGCAGTTGTGGCAAGAACGCCAGCTCAGAATGAACACACCCACCAAGA
GCCTCCTTGTTTCATAACCACAGGTTACCCTACAAACCACTGTCCCCACACAACCCTGGGGAT
GTTTTTAAACACACACCTCTAACGCATATCTTACAGTCACTGTTGTCTTGCCTGAGGGTTGA
ATTTTTTTTAAATGAAAGTGCAATGAAATCACTGGATTAAATCCTACGGACACAGAGCTGAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 188

MNTWLLFLPLFPVQVQTLIVVIGMLVLLLDLGLVHLGQLLIFHIYLSMSPTLSPRSPQGW
VVRAAHLTPLLEYVPNPEPPTPGARVFVPRVRMCSGSASPRSEIMDKKGKSQEEIKSMRTQQ
AQQEAELTPRPAGVVPGA

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FIGURE 189

GGAGTGCAGATGGCATCCTTCGGTTCCTCCAGACAAGCTGCAAGACGCTGACCATGGCCAAAG
ATGGAGCTCTCGAAGGCCTTCTCTGGCCAGCGGACACTCCTATCTGCCATCCTCAGCATGCT
ATCACTCAGCTTCTCCACAACATCCCTGCTCAGCAACTACTGGTTTGTGGGCACACAGAAGG
TGCCCAAGCCCCTGTGCGAGAAAGGTCTGGCAGCCAAGTGCTTTGACATGCCAGTGTCCTTG
GATGGAGATACCAACACATCCACCCAGGAGGTGGTACAATACAACCTGGGAGACTGGGGATGA
CCGGTTCTCCTTCCGGAGCTTCCGGAGTGGCATGTGGCTATCCTGTGAGGAACTGTGGAAG
AACCAGGGGAGAGGTGCCGAAGTTTCATTGAACTTACACCACCAGCCAAGAGAGGTGAGAAA
GGACTACTGGAATTTGCCACGTTGCAAGGCCCATGTACCCCCACTCTCCGATTTGGAGGGAA
GCGGTTGATGGAGAAGGCTTCCCTCCCCCTCCCCCTCCCTTGGGGCTTTGTGGCAAAAATCCTA
TGGTTATCCCTGGGAACGCAGATCACCTACATCGGACTTCAATTCATCAGCTTCCTCCTGCT
ACTAACAGACTTGCTACTCACTGGGAACCCTGCCTGTGGGCTCAAACCTGAGCGCCTTTGCTG
CTGTTTTCTCTGTCTGTGCTCAGGTCTCCTGGGGATGGTGGCCACATGATGTATTACAAGTC
TTCCAAGCGACTGTCAACTTGGGTCCAGAAGACTGGAGACCACATGTTTGGAATTATGGCTG
GGCCTTCTACATGGCCTGGCTCTCCTTCACCTGCTGCATGGCGTCGGCTGTCAACCACCTTCA
ACACGTACACCAGGATGGTGCTGGAGTTCAAGTGCAAGCATAGTAAGAGCTTCAAGGAAAAC
CCGAAGTGCCTACCACATCACCATCAGTGTTTCCCTCGGCGGCTGTCAAGTGCAGCCCCAC
CGTGGGTCCTTTGACCAGCTACCACCAGTATCATAATCAGCCCATCCACTCTGTCTCTGAGG
GAGTCGACTTCTACTCCGAGCTGCGGAACAAGGGATTTCAAAGAGGGGGCCAGCCAGGAGCTG
AAAGAAGCAGTTAGGTCATCTGTAGAGGAAGAGCAGTGTTAGGAGTTAAGCGGGTTTGGGGA
GTAGGCTTGAGCCCTACCTTACACGTCTGCTGATTATCAACATGTGCTTAAGCCAACATCCG
TCTCTTGAGCATGGTTTTTTAGAGGCTACGAATAAGGCTATGAATAAGGGTTATCTTTAAGTC
CTAAGGGATTCTGGGTGCCACTGCTCTCTTTTCTCTACAGCTCCATCTTGTTTCACCCAC
CCCACATCTCACACATCCAGAATTCCCTTCTTTACTGATAGTTTCTGTGCCAGGTCTGGGC
TAAACCATGGAGATAAAAAGAAGAGTAAAATACACTTCCCGACCTTAAGGATCTGAAA

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FIGURE 190

MAKMELSKAFSGQRTLLSAILSMLSLSFSTTSLLSNYWFVGTQKVPKPLCEKGLAAKCFDMP
VSLDGDNTNTSTQEVVQYNWETGDDRFSSFRSFRSGMWLSCEETVEEPGERCRSFIELTPPAKR
GEKGLLEFATLQGPCHPTLRFGGKRLMEKASLPSPPLGLCGKNPMVIPGNADHLHRTSIHQL
PPATNRLATHWEPCLWAQTERLCCCFLCPVRSPGDGGPHDVFTSLPSDCQLGSRRLTTTCLE
LWLGLLHGLALLHLLHGVGCHHLQHVVHVDGAGVQVQA

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FIGURE 192

MWLPLGLLSLCLSPLPILSSPSLKSQACQQLLWTLPSPLVAFRANRTTYVMDVSTNQGSME
HRNHLCFCDLYDRATSPPLKCSLL

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FIGURE 193

GTAGCGCGTCTTGGGTCTCCCGGCTGCCGCTGCTGCCGCCGCCGCTCGGGTCGTGGAGCCAGGAGCGACGTCA
 CCGCC**ATG**GCCAGGCATCAAAGCTTTGATTAGTTTGTCTTTGGAGGAGCAATCGGACTGATGTTTTTGATGCTT
 GGATGTGCCCTTCCAATATACAACAAATACTGGCCCCCTCTTTGTTCTATTTTTTTTACATCCTTTACCTATTCC
 ATACTGCATAGCAAGAAGATTAGTGGATGATACAGATGCTATGAGTAACGCTTGTAAGGAACCTGCCATCTTTC
 TTACAACGGGCATTGTCTGTCTAGCTTTTGGACTCCCTATTGTATTTGCCAGAGCACATCTGATTGAGTGGGA
 GCTTGTGCACCTGTTCTCACAGGAAACACAGTCATCTTTGCAACTATACTAGGCTTTTTCTTGGTCTTTGGAAG
 CAATGACGACTTCAGCTGGCAGCAGTGG**TGA**AAAGAAATTACTGAACTATTGTCAAATGGACTTCCTGTCATTT
 GTTGGCCATTACGCACACAGGAGATGGGGCAGTTAATGCTGAATGGTATAGCAAGCCTCTTGGGGTATTTTA
 GGTGCTCCCTTCTCACTTTTATTGTAAGCATACTATTTTTCACAGAGACTTGCTGAAGGATTTAAAGGATTTTCT
 CTTTTGGAAAAGCTTGACTGATTTTCACTATCTATAGTATGCTTTTTTGTGGTGTCTGCTGAATTTAAATAT
 TTATGTGTTTTTCTGTTAGGTTGATTTTTTTTGAATCAATATGCAATGTTAAACACTTTTTTAATGTAATCA
 TTTGCATTGGTTAGGAATTCAGAATTCGCCCGGCTCTATTACTGGTCAAGTACATCTTTTCTCTTAAATATTAT
 TAGCCTCCATTATTACAAAAAATTATAAAAAATAAGTTTTTCAGTCAGTCAGGATGACATCACTCCCAATGTTATG
 CAGACATACAGACGGTTGGCATACTGTTATAGACTGTATACTCAGTGCAAATATAGCTGCATTTATACCTCAGAG
 GGGCCAAGTGTTAATGCCATGCCCTCCGTTAAGGGTTGTGGTTTTACTGGTAGACAGATGTTTTGTGGATTG
 AAAATTATTTTATGGAATTGCTACAGAGGAGTGCTTTTCTTCTCAATTGTTAGAAGAATTTATGTTAAACTTTA
 AGGTAAGGGTGTA AAAACATTTTTGAGATAAGGTTTTTATTTATGTTTATTATTGTTAGAGTGAGTTGCAATGT
 GGGAGAAGATGACATTGAAATTCAGTTTTTGAATCCTGTTTCTATTTATAAGTGAAATTTGTGATCTCCTATC
 AACCTTTTCATGTTTTACCCTGTTAAATGGACATACATGGAACCACTACTGATGAGGGACAGTTGTATGTTTGC
 ATCATATATGCCAGAAAACCTTCTCTGCTTCCCTCTTTGACTTATTTGGTATGTTGTATATATTACATAAAAA
 TAACTTTTCAAATATAGTTTAAATAACACTTAGAAGTGTTTACTTACCTGGAAAATAATTGCTATGCCGTACATT
 CAGAGTGCCCCCTCCCCTGCAAGGCCTTGCCATGATTAACAAGTAACCTTGTTAGTCTTACAGATAATTCATGCA
 TTAACAGTTTAAGATTTAGACCATGGTAATAGTAGTCTTATTCTCTAAGGTTATATCATATGTAATTTAAAG
 TATTTTTAAGACAAGTTTCTGTATACCTCTGAAGTGTGTTTGTATTTGAGTTCATCATGATAGATCTGCTGTTT
 CCTTATAAAAGGCATTTGTTGTGTGAGTTAATGCAAAGTAGCCAAGTCCAGCTATATAGCAGCTTCAGAAACAT
 ACCTGACCAAAAAATTCCCAGTAACCAGGCATGATCAATTTATAGTGGTCGTTTACATCTAATAATTATCAGGA
 CTTTTTTTCAGGAGTGGGTATATAAAAAACATTCAAGTTGGTCTGACAGTATTTTGTAAAGGATATTTGTTGTATG
 TTTATTCAGTATACTTACATAAAAAATTATTTGCCATCAGCCAAAACCTCAGTAATCATGACAGCTGTCTGTTGT
 TTTATGAAGTTTATTTCTCAAGAAAATGGGAATAAATTTGGGATTTGTTTCACTTTTTTACTAAAGATGCCTAA
 AGCCACAGGTTTTATTGCCTAACTTAAGCCATGACTTTTAGATATGAGATGACGGGAAGCAGGACGAAATATCG
 GCGTGTGGCTGGAGCCTTCCCCTGGAGGCTGAAAGTGGCTTGTTGTTATATAATGTTTCAAGAGGAA
 GGTGCAGGTACACATGAGTTAGAGAGCTGGTGAGACAGTTGGGAACCTTTTGTGCTTGTGATCTACTGGACTTT
 TTTTTTGCAGGAAGTGCACTTCTCTGGTCCCTTCCCTATTTTCTGTTCTGGATGTCAGTGCAGTGCAGTGCCTACTG
 TTTTATCCACTTGGCCACAGACTTTTTCTAACAGCTGCGTATTATTTCTATATACTAATTGCATTGGCAGCATT
 GTGTCTTTGACCTTGATACTAGCTTGACATAGTGCTGTCTCTGATTTCTAGGCTAGTTACTTGAGATATGAAT
 TTTCCATAGAATATGCACTGATACAACATTACCATTCTTCTATGGAAAGAAAACCTTTTGATGATGAAACAATAA
 AGATTTTTAAATATCTATTTTAAAAA

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FIGURE 194

MAGIKALISLSFGGAIGLMFLMLGCALPIYNKYWPLFVLFFYILSPIPYCIARRLVDDTDAM
SNACKELAIFLTGTGIVVSAFGLPIVFARAHLEWGACALVLTGNTVIFATILGFFLVFGSND
DFSWQQW

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[illegible]

MDFULLGLCLYWLRLRRPSGVVLCLLGACFQMLPAAPSGCPQLCRCEGRLLYCEALNLTEAPH
NLSGLLGLSLRYNSLSELRAGQFTGLMQLTWLYLDHNHICSVQGDAFQKLRRVKELTLSSNQ
ITQLPNTTFRMPNLRVDSLYNKLQALAPDLFHGLRKLTTLHMRANAIQFVPVRI FQDCRS
LKFLDIGYNQLKSLARNSFAGLFKLTELHLEHNDLVKVNFAHFPRLLISLHSLCLRRNKVAIV
VSSLDWVWNLEKMDLSGNEIEYMEPHVFETVPHLQSLQLDSNRLTYIEPRILNSWKSLSIT
LAGNLWDCGRNVCALASWLSNFQGRYDGNLQCASPEYAQGEDVLDVYAFHLCEDGA EPTSG
HLLSAVTNRSDLGPPASSATT LADGGEGQHDGTFEPATVALPGGEHAENAVQIHKVVTGTMA
LIFSFLIVVLVLYVSWKCFPASLRQLRQCFVTQRRKQKQKQTMHQMAAMSAQEYYVDYKPNH
IEGALVIINEYGSCTCHQQPARECEV

GTGCAAGGAGCCGAGGCGAGATGGGCGTCTCTGGGCCGGGTCTCTGCTGTGGCTGCAGCTCTGC
GCACTGACCCAGGCGGTCTCCAACTCTGGGTCCCCAACACGGACTTCGACGTTCGACGCCAA
CTGGAGCCAGAACCGGACCCCGTTCGCGCCGGCGGGCGCCGTTGAGTTCCCGGCGGACAAGATGG
TGTCACTCCTGGTGAAGAAGGTCACGCCGTCTCAGACATGCTCCTGCCGTGGATGGGGAA
CTCGTCTCTGGCTTCAGGAGCCGGATTCGGCGTCTCAGACGTGGGCTCGCACCTGGACTGTGG
CGCGGGCGAACCTGCCGTCTTCCGCGACTCTGACCGCTTCTCCTGGCATGACCCGCACCTGT
GGCGCTCTGGGGACGAGGCACCTGGCCTCTTCTTCGTGGACGCCGAGCGCGTGCCCTGCCGC
CACGACGACGTCTTCTTTCCGCCTAGTGCCTCCTTCCGCGTGGGGCTCGGCCCTGGCGCTAG
CCCCGTGCGTGTCCGCAGCATCTCGGCTCTGGGCCGGACGTTACGCGCGACGAGGACCTGG
CTGTTTTCTCTGGCGTCCCGCGCGGGCCGCCTACGCTTCCACGGGCCGGGCGCGCTTGAGCGTG
GGCCCCGAGGACTGCGCGGACCCGTTCGGGCTGCGTCTGCGGCAACGCGGAGGCGCAGCCGTG
GATCTGCGCGGCCCTGCTCCAGCCCCCT

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FIGURE 198

MGVLGRVLLWLQLCALTQAVSKLWVPNTDFDVAANWSQNRTPCAGGAVEFPADKMVSVLVQE
GHAVSDMLLPLDGELVLASGAGFGVSDVGSHLDCGAGEPAVFRDSDRFSWHDPHLWRSGDEA
PGLFFVDAERVPCRHDDVFFPPSASFRVGLGPGASPVVRVSISALGRTFTRDEDLAVFLASR
AGRLRFHGPALSVGPEDCADPSGCVCGNAEAQPWICAALLQP

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FIGURE 199

ATCGCATCAATTGGGAGTACCATCTTCCTCATGGGACCAGTGAAACAGCTGAAGCGAATGTT
TGAGCCTACTCGTTTGATTGCAACTATCATGGTGCTGTTGTGTTTTGCACTTACCCTGTGTT
CTGCCTTTTGGTGGCATAACAAGGGACTTGCACTTATCTTCTGCATTTTGCAGTCTTTGGCA
TTGACGTGGTACAGCCTTTCCTTCATACCATTGCAAGGGATGCTGTGAAGAAGTGTTTGC
CGTGTGTCTTGCATAATTTCATGGCCAGTTTTATGAAGCTTTGGAAGGCACTATGGACAGAAG
CTGGTGGACAGTTTTGTAACCTATCTTCGAAACCTCTGTCTTACAGACATGTGCCTTTTATCT
TGCAGCAATGTGTTGCTTGTGATTGCAACATTTGAGGGTTACTTTTGAAGCAACAATACAT
TCTCGAACCTGAATGTCAGTAGCACAGGATGAGAAGTGGGTTCTGTATCTTGTGGAGTGGAA
TCTTCCTCATGTACCTGTTTCCTCTCTGGATGTTGTCCCACTGAATTCCCATGAATACAAAC
CTATTCAGCAACAGCAA
AAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 200

MGPVKQLKRMFEPTRLIATIMVLLCFALTLCSAFWWHNKGLALIFCILQSLALTWYSLSFIP
FARDAVKKCFVCLA

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FIGURE 201

TTGAGCGCAGGTGAGCTCCTGCGCGTTCCGGGGGCGTTCCCTCCAGTCACCCCTCCCGCCGTTACCCGCGGCGCGC
 CCGAGGGAGTCTCCTCCAGACCCCTCCCTCCCGTTGCTCCAACTAATACGGACTGAACGGATCGCTGCGAGGGT
 GGGAGAGAAAATTAGGGGGAGAAAGGACAGAGAGCAACTACCATCCATAGCCAGATAGATTATCTTACACTG
 AACTGATCAAGTACTTTGAAAATGACTTCGAAATTTATCTTGGTGTCTTCATACTTGCTGCACTGAGTCTTTC
 AACCACCTTTTCTCTCCAACCTAGACCAGCAAAAGGTTCTACTAGTTTCTTTTGATGGATTCCGTTGGGATTACT
 TATATAAAGTTCCAACGCCCCATTTTCATTATATTATGAAATATGGTGTTCACGTGAAGCAAGTTACTAATGTT
 TTTATTACAAAACCTACCCTAACCATTTACTTTGGTAAGTGGCCTCTTTCAGAGAAATCATGGGATTGTTGC
 AAATGATATGTTTGATCCTATTCGGAACAAATCTTCTCCTTGGATCACATGAATATTTATGATTCCAAGTTTT
 GGGGAAGAAGCGACACCAATATGGATCACAAACCAGAGGGCAGGACATACTAGTGGTGCAGCCATGTGGCCCGGA
 ACAGATGTAAAAATACATAAGCGCTTTCCTACTCATTACATGCCTTACAATGAGTCAGTTTCATTTGAAGATAG
 AGTTGCCAAAATTGTTGAATGGTTTACGTCAAAAGAGCCCATAAATCTTGGTCTTCTCTATTGGGAAGACCCTG
 ATGACATGGGCCACCATTTGGGACCTGACAGTCCGCTCATGGGGCCTGTCAATTCAGATATTGACAAGAAGTTA
 GGATATCTCATACAAATGCTGAAAAAGGCAAAGTTGTGGAACACTCTGAACCTAATCATCACAAAGTGATCATGG
 AATGACGCAGTGCTCTGAGGAAAGGTTAATAGAACTTGACCAGTACCTGGATAAAGACCCTATACCCCTGATTG
 ATCAATCTCCAGTAGCAGCCATCTTGCCAAAAGAAGGTAAATTTGATGAAGTCTATGAAGCACTAACTCAGCT
 CATCCTAATCTTACTGTTTACAAAAAAGAAGACGTTCCAGAAAGGTGGCATTACAAATACACAGTCCGAATTCA
 ACCAATCATAGCAGTGGCTGATGAAGGTGGCACATTTTACAGAATAAGTCAGATGACTTTCTGTTAGGCAACC
 ACGGTTACGATAATGCGTTAGCAGATATGCATCCAATATTTTTAGCCCATGGTCCTGCCTTCAGAAAGAATTTTC
 TCAAAAGAAGCCATGAACCTCCACAGATTTGTACCCACTACTATGCCACCTCCTCAATATCACTGCCATGCCACA
 CAATGGATCATTCTGGAATGTCCAGGATCTGCTCAATTCAGCAATGCCAAGGGTGGTCCCTTATACACAGAGTA
 CTATACTCCTCCCTGGTAGTGTTAAACCAGCAGAATATGACCAAGAGGGGTCAATACCCTTATTTCATAGGGGTC
 TCTCTTGGCAGCATTATAGTGATTGTATTTTTTTGTAATTTTCAATTAAGCATTTAATTCACAGTCAAATACCTGC
 CTTACAAGATATGCATGCTGAAATAGCTCAACCATTATTACAAGCCTAATGTTACTTTGAAGTGGATTTCATA
 TTGAAGTGGAGATTCCATAATTATGTCAGTGTTTAAAGGTTTCAAATTCCTGGGAACCAGTTCCAAACATCTGC
 AGAAACCATTAAGCAGTTACATATTTAGGTATACACACACACACACACACATACACACACACGGACCAAAA
 ATACTTACACCTGCAAAGGAATAAAGATGTGAGAGTATGTCTCCATTGTTCACTGTAGCATAGGGATAGATAAG
 ATCCTGCTTTATTTGGACTTGGCGCAGATAATGTATATATTTAGCAACTTTGCACTATGTAAAGTACCTTATAT
 ATTGCACTTTAAATTTCTCTCCTGATGGGTACTTTAATTTGAAATGCACTTTATGGACAGTTATGTCTTATAAC
 TTGATTGAAAATGACAACTTTTTGCACCCATGTACAGAAATACTTGTTACGCATTGTTCAAACCTGAAGGAAATT
 TCTAATAATCCCGAATAATGAACATAGAAATCTATCTCCATAAATTGAGAGAAGAAGAAGGTGATAAGTGTGGA
 AAATTAAATGTGATAACCTTTGAACCTTGAATTTTGGAGATGTATCCCAACAGCAGAAATGCAACTGTGGGCAT
 TTCTTGTCTTATTTCTTTCCAGAGAACGTGGTTTTTCATTTATTTTTCCCTCAAAGAGAGTCAAATACTGACAG
 ATTGCTTCTAAATATATTGTTTCTGTCATAAAATTAATGTGATTTCTGATGAGTCATATTACTGTGATTTTCA
 TAATAATGAAGACACCATGAATATACTTTTTCTTCTATATAGTTTACGCAATGGCCTGAATAGAAGCAACCAGGCA
 CCATCTCAGCAATGTTTTCTTGTGTAATTATTTGCTCCTTTGAAAATTAATCACTATTAATTACATTAA
 AAATCAAATTGGATAAAAAAAAAAAAAAAAAAAAA

MTSKFILVSFILAAALSLSTTFSLQLDQQVLLVVSFDGFRWDYLYKVPTPHFHYIMKYGVHVK
QVTNVFITKTYPNHYTLVTGLFAENHGIVANDMFDPIRNKSFSLSLDMNIYDSKFWEETPIW
ITNQ RAGHTSGAAMWPGTDVKIHKRFPTHYMPYNESVSFEDRVAKIVWFTSKEPINLGLLY
WEDPDDMGHHLGPDSPLMGPVISDIDKKLGYLIQMLKKAKLWNTNLNIITSDHGMTQCSEER
LIELDQYLDKDHYTELIDQSPVAAILPKEGKFDEVYEALTHAHPNLTVYKKEDVPERWHYKYN
SRIQPIIAVADEGWHLQNKSDDFLLGNHGYDNALADMHPIFLAHGPAFRKNFSKEAMNSTD
LYPLLCHLLNITAMPHNGSFWNVQDLLNSAMPRVVPYTQSTILLPGSVKPAEYDQEGSYPFY
IGVSLGSIIVIVFFVIFIKHLIHSQIPALQDMHAEIAQPLLQA

amino acids 1-22

amino acids 429-452

amino acids 101-104, 158-161, 292-295, 329-332, 362-365, 369-372, 382-385, 389-392

amino acids 69-85

amino acids 212-241

FIGURE 203

GGATTTTTGTGATCCGCGATTTCGCTCCACGGGCGGGACCTTTGTAAGTGCAGGGAGGCCCAG
GACAGGCCCACCCTGCGGGGCGGGAGGCAGCCGGGGTGAGGGAGGTGAAGAAACCAAGACGC
AGAGAGGCCAAGCCCCTTGCCTTGGGTACACAGCCAAAGGAGGCAGAGCCAGAACTCACAA
CCAGATCCAGAGGCAACAGGGAC**ATG**GCCACCTGGGACGAAAAGGCAGTCACCCGCAGGGCC
AAGGTGGCTCCCGCTGAGAGGATGAGCAAGTTCTTAAGGCACTTCACGGTCGTGGGAGACGA
CTACCATGCCTGGAACATCAACTACAAGAAATGGGAGAATGAAGAGGAGGAGGAGGAGGAGG
AGCAGCCACCACCCACACCAGTCTCAGGCGAGGAAGGCAGAGCTGCAGCCCCCTGACGTTGCC
CCTGCCCCCTGGCCCCGCACCCAGGGCCCCCCTTGACTTCAGGGGCATGTTGAGGAAACTGTT
CAGCTCCACAGGTTTCAGGTCATCATCATCTGCTTGGTGGTTCTGGATGCCCTCCTGGTGC
TTGCTGAGCTCATCCTGGACCTGAAGATCATCCAGCCCGACAAGAATAACTATGCTGCCATG
GTATTCACACTACATGAGCATCACCATCTTGGTCTTTTTTATGATGGAGATCATCTTTAAATT
ATTTGTCTTCCGCCTGAGTTCTTTCACCACAAGTTTGAGATCCTGGATGCCCCGTCGTGGTGG
TGGTCTCATTCATCCTGGACATTGTCCTCCTGTTCCAGGAGCACCAGTTTGAGGCTCTGGGC
CTGCTGATTCTGCTCCGGCTGTGGCGGGTGGCCCGGATCATCAATGGGATTATCATCTCAGT
TAAGACACGTTTCAAGACGGCAACTCTTAAGGTTAAAACAGATGAATGTACAATTGGCCGCCA
AGATTCAACACCTTGAGTTCAGCTGCTCTGAGAAGCCCCCTGGAC**TGA**TGAGTTTGCTGTATC
AACCTGTAAGGAGAAGCTCTCTCCGGATGGCTATGGGAATGAAAGAATCCGACTTCTACTCT
CACACAGCCACCGTGAAAGTCCTGGAGTAAATGTGCTGTGTACAGAAGAGAGAGAAGGAAG
CAGGCTGGCATGTTCACTGGGCTGGTGTACGACAGAGAACCTGACAGTCACTGGCCAGTTA
TCACTTCAGATTACAAATCACACAGAGCATCTGCCTGTTTTCAATCACAAGAGAACAAAACC
AAAATCTATAAAGATATTCTGAAAATATGACAGAATTTGACAAATAAAAGCATAAACGTGTA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 204

MATWDEKAVTRRAKVAPAERMSKFLRHFTVVGDDYHAWNINYKKWENEEEEEEQPPPTPV
SGEEGRAAAPDVAPAPGPAPRAPLDFRGMLRKLFSSSHRFQVIIICLVVLDALLVLAELILD
KIIQPDKNNYAAMVFHYMSITILVFFMMEIIFKLFVFRLLSSFTTSLRSWMPVVVVVSFILD
VLLFQEHQFEALGILLILLRLWRVARIINGIIISVKTRSERQLLRLQMNVQLAAKIQHLEFS
CSEKPLD

FIGURE 206

MLCLCLYVPVIGEAQTEFQYFESKGLPAELKSIFKLSVFIPSQEFSTYRQWKQKIVQAGDKD
LDGQLDFEEFVHYLQDHEKKLRLVFKILDKKNDGRIDAQEIMQSLRDLGVKISEQQAEEKILK
SMDKNGTMTIDWNEWRDYHLLHPVENIPEIILYWKHSTIFDVGENLTVPDEFTVEERQTGMW
WRHLVAGGGAGAVSRTCTAPLDRLKVLMOVHASRSNNMGIVGGFTQMIREGGARSLWRGNGI
NVLKIAPESAIKFMAYEQIKRLVGSQETLRIHERLVAGSLAGAIAQSSIYPMEVLKTRMAL
RKTGQYSGMLDCARRILAREGVAAFYKGYVPNMLGIIPYAGIDLAVYETLKNAWLQHYAVNS
ADPGVFVLLACGTMSSTCGQLASYPLALVRTRMQAQASIEGAPEVTMSSLFKHILRTEGAFG
LYRGLAPNFMKVIPAVSISYVVYENLKITLGVQSR

Important features:

Signal peptide:

amino acids 1-16

Transmembrane domain:

amino acids 284-304, 339-360, 376-394

Mitochondrial energy transfer proteins signature.

amino acids 206-215, 300-309

N-glycosylation site.

amino acids 129-133, 169-173

Elongation Factor-hand calcium-binding protein.

amino acids 54-73, 85-104, 121-140

[illegible]

FIGURE 209

GAATTTGTAGAAGACAGCGGCGTTGCC**ATG**GCGGCGTCTCTGGGGCAGGTGTTGGCTCTGGT
GCTGGTGGCCGCTCTGTGGGGTGGCACGCAGCCGCTGCTGAAGCGGGCCTCCGCCGGCCTGC
AGCGGGTTCATGAGCCGACCTGGGCCCAGCAGTTGCTACAGGAGATGAAGACCCTCTTCTTG
AATACTGAGTACCTGATGCCCTTTCTCCTCAACCAGTGTGGATCCCTTCTCTATTACCTCAC
CTTGGCATCGACAGATCTGACCCTGGCTGTGCCCATCTGTAACTCTCTGGCTATCATCTTCA
CACTGATTGTTGGGAAGGCCCTTGGAGAAGATATTGGTGGAAAACGTAAGTTAGACTACTGC
GAGTGCGGGACGCAGCTCTGTGGATCTCGACATACCTGTGTAGTTCCTTCCCAGAACCCAT
CTCCCCAGAGTGGGTGAGGACACGGCCTTTTCCCATCCTGCCCTTTCCTCTGCAGCTGTTTT
GCTTCCCTGTGGCCATCAGAGTTCCCTTCCCCTGGACAGTCTGGAGAAAGACAGAGGCTGGG
GTTTGGGAT**TGA**AGACCAGACCCCATCTGAGCCCTTCCCTCCAGCCCTGTACCAGCTCCTACT
GGCATGGCTGAGCTCAGACCCTCCTGATTTCTGCCTATTATCCCAGGAGCAGTTGCTGGCAT
GGTGCTCACCGTGATAGGAATTTCACTCTGCATCACAAGCTCAGTGAGTAAGACCCAGGGGC
AACAGTCTACCCTTTGAGTGGGCCGAACCCACTTCCAGCTCTGCTGCCTCCAGGAAGCCCCT
GGGCCATGAAGTGCTGGCAGTGAGCGGATGGACCTAGCACTTCCCCTCTCTGGCCTTAGCTT
CCTCCTCTCTTATGGGGATAACAGCTACCTCATGGATCACAATAAGAGAACAAGAGTGAAAG
AGTTTTGTAACCTTCAAGTGCTGTTCACTGCTGCGGGGATTAGCACAGGAGACTCTACGCTCA
CCCTCAGCAACCTTTCTGCCCCAGCAGCTCTCTTCCCTGCTAACATCTCAGGCTCCCAGCCCA
GCCACCATTA CTGTGGCCTGATCTGGACTATCATGGTGGCAGGTTCATGGACTGCAGAACT
CCAGCTGCATGGAAAGGGCCAGCTGCAGACTTTGAGCCAGAAATGCAAACGGGAGGCCTCTG
GACTCAGTCAGAGCGCTTTGGCTGAATGAGGGGTGGAACCGAGGGAAGAAGGTGCGTCGGA
GTGGCAGATGCAGGAAATGAGCTGTCTATTAGCCTTGCTGCCCCACCCATGAGGTAGGCAG
AAATCCTCACTGCCAGCCCCCTTTAAACAGGTAGAGAGCTGTGAGCCCCAGCCCCACCTGAC
TCCAGCACACCTGGCGAGTAGTAGCTGTCAATAAATCTATGTAAACAGACAAAAAAAAAAAAA
AAA

Figure 1 consists of 12 bar charts, each representing a different protein type (I through XII). Each chart shows the percentage of total protein in various fractions (A through L) under different conditions (1 through 12). The y-axis for all charts represents the percentage of total protein, ranging from 0 to 100. The x-axis for each chart represents the protein type. The legend indicates that the bars represent the percentage of total protein in each fraction.

| Protein Type | Fraction | Condition 1 | Condition 2 | Condition 3 | Condition 4 | Condition 5 | Condition 6 | Condition 7 | Condition 8 | Condition 9 | Condition 10 | Condition 11 | Condition 12 |
|--------------|----------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|--------------|--------------|--------------|
| I | A | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 |
| | B | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 |
| | C | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 |
| | D | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 |
| | E | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 |
| | F | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 |
| | G | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 |
| | H | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 |
| | I | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 |
| | J | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 |
| | K | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 |
| | L | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 |
| II | A | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 |
| | B | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 |
| | C | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 |
| | D | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 |
| | E | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 |
| | F | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 |
| | G | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 |
| | H | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 |
| | I | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 |
| | J | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 |
| | K | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 |
| | L | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 |
| III | A | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 |
| | B | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 |
| | C | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 |
| | D | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 |
| | E | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 |
| | F | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 |
| | G | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 |
| | H | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 |
| | I | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 |
| | J | 10 | 10 | 10 | 10 | 10 | | | | | | | |

FIGURE 210

MAASLGQVLALVLVAALWGGTQPLLKRASAGLQRVHEPTWAQQLQEMKTLFLNTEYLMPF
LNQCGSLLYYLTLASTDLTLAVPICNSLAIIFTLIVGKALGEDIGGKRKLDYCECGTQLCGS
RHTCVSSFPEPISPFWVRTRPFPILPFFPLQLFCFLVAIRVPFPWTVVRKTEAGVWD

FIGURE 211

CTTCTGTAGGACAGTCACCAGGCCAGATCCAGAAGCCTCTCTAGGCTCCAGCTTTCTCTGTG
GAAGATGACAGCAATTATAGCAGGACCCTGCCAGGCTGTGCGAAAAGATTCCGCAATAAACT
TTGCCAGTGGGAAGTACCTAGTGAAACGGCCTAAGATGCCACTTCTTCTCATGTCCCAGGCT
TGAGGCCCTGTGGTCCCCATCCTTGGGAGAAGTCAGCTCCAGCACCA**ATGA**AGGGCATCCTCG
TTGCTGGTATCACTGCAGTGCTTGTGTCAGCTGTAGAATCTCTGAGCTGCGTGCAGTGTAAT
TCATGGGAAAAATCCTGTGTCAACAGCATTGCCTCTGAATGTCCCTCACATGCCAACACCAG
CTGTATCAGCTCCTCAGCCAGCTCCTCTCTAGAGACACCAGTCAGATTATACCAGAATATGT
TCTGCTCAGCGGAGAACTGCAGTGAGGAGACACACATTACAGCCTTCACTGTCCACGTGTCT
GCTGAAGAACACTTTTCATTTTGTAAAGCCAGTGCTGCCAAGGAAAGGAATGCAGCAACACCAG
CGATGCCCTGGACCCTCCCCTGAAGAACGTGTCCAGCAACGCAGAGTGCCCTGCTTGTTATG
AATCTAATGGAACCTTCTGTGCTGGGAAGCCCTGGAAATGCTATGAAGAAGAACAGTGTGTC
TTTCTAGTTGCAGAACTTAAGAATGACATTGAGTCTAAGAGTCTCGTGCTGAAAGGCTGTTC
CAACGTCAGTAACGCCACCTGTGAGTTTCTGTCTGGTGAACAAGACTCTTGGAGGAGTCA
TCTTTCGAAAGTTTGAGTGTGCAATGTAAACAGCTTAACCCCCACGTCTGCACCAACCACT
TCCCACAACGTGGGCTCCAAAGCTTCCCTCTACCTCTTGGCCCTTGCCAGCCTCCTTCTTCG
GGGACTGCTGCCC**TGA**GGTCTTGGGGCTGCACTTTGCCAGCACCCCATTTCTGCTTCTCTG
AGGTCCAGAGCACCCCCTGCGGTGCTGACACCCTCTTTCCTGCTCTGCCCCGTTTAACTGC
CCAGTAAGTGGGAGTCACAGGTCTCCAGGCAATGCCGACAGCTGCCTTGTTCTTCATTATTA
AAGCACTGGTTCATTCACTGCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 212

MKGILVAGITAVLVAAVESLSCVQCNSWEKSCVNSIASECPSHANTSCISSSASSSLETPVR
LYQNMFCSAENCSEETHITAFTVHVSAEEHFHFVSQCCQGKECSNTSDALDPPLKNVSSNAE
CPACYESNGTSCRGPWKCYEEEQCVFLVAELKNDIESKSLVLKGCSNVSNATCQFLSGENK
TLGGVIFRKFEKANVNSLTPTSAPTTSBNVGSKASLYLLALASLLLRGLLP

Figure 212

FIGURE 213

GGCCTCGGTTCAAACGACCCGGTGGGTCTACAGCGGAAGGGAGGGAGCGAAGGTAGGAGGCA
GGGCTTGCCTCACTGGCCACCCTCCCAACCCCAAGAGCCCAGCCCC**ATG**GTCCCCGCCGCCG
GCGCGCTGCTGTGGGTCTGCTGCTGAATCTGGGTCCCCGGGCGGCGGGGGCCCAAGGCCTG
ACCCAGACTCCGACCGAAATGCAGCGGGTCAGTTTACGCTTTGGGGGCCCCATGACCCGCAG
CTACCGGAGCACCGCCCGGACTGGTCTTCCCCGGAAGACAAGGATAATCCTAGAGGACGAGA
ATGATGCCATGGCCGACGCCGACCGCCTGGCTGGACCAGCGGCTGCCGAGCTCTTGGCCGCC
ACGGTGTCCACCGGCTTTAGCCGGTCGTCCGCCATTAACGAGGAGGATGGGTCTTCAGAAGA
GGGGGTGTGATTAATGCCGGAAGGATAGCACCAGCAGAGAGCTTCCCAGTGCGACTCCCA
ATACAGCGGGGAGTTCCAGCACGAGGTTTATAGCCAATAGTCAGGAGCCTGAAATCAGGCTG
ACTTCAAGCCTGCCGCGCTCCCCGGGAGGTCTACTGAGGACCTGCCAGGCTCGCAGGCCAC
CCTGAGCCAGTGGTCCACACCTGGGTCTACCCCGAGCCGGTGGCCGTACCCTCACCCACAG
CCATGCCATCTCCTGAGGATCTGCGGCTGGTGCTGATGCCCTGGGGCCCGTGGCACTGCCAC
TGCAAGTCGGGCACCATGAGCCGGAGCCGGTCTGGGAAGCTGCACGGCCTTCCGGGCGCCT
TCGAGTTGGGGCGCTGAGCCAGCTCCGCACGGAGCACAAGCCTTGACCTATCAACAATGTC
CCTGCAACCGACTTCGGGAAGAGTGCCCCCTGGACACAAGTCTCTGTACTGACACCAACTGT
GCCTCTCAGAGCACCACCAGTACCAGGACCACCACTACCCCTTCCCCACCATCCACCTCAG
AAGCAGTCCCAGCCTGCCACCCGCCAGCCCCTGCCAGCCCTGGCTTTTTGGAAACGGGTCA
GGATTGGCCTGGAGGATATTTGGAATAGCCTCTCTTCAGTGTTACAGAGATGCAACCAATA
GACAGAAACCAGAGG**TAA**TGGCCACTTCATCCACATGAGGAGATGTCAGTATCTCAACCTCT
CTTGCCCTTTCAATCCTAGCACCCACTAGATATTTTTAGTACAGAAAAACAAAACCTGGAAAA
CACAA

FIGURE 214

MVPAAGALLWVLLLNLPRAAGAQGLTQTPTEMQRVSLRFGGPMTRSyrSTARTGLPRKTRI
ILEDENDAMADADRLAGPAAAEALLAATVSTGFSRSSAINEEDGSSEEGVINAGKDSTSREL
PSATPNTAGSSSTRFIANSQEPEIRLTSSLPRSPGRSTEDLPGSQATLSQWSTPGSTPSRWP
SPSPTAMPSPEDLRLVLMWPWGPWHCHCKSGTMSRSRSGKLHGLSGRLRVGALSQLRTEHKPC
TYQQCPCNRLREECPLDTSLCDTNCASQSTTSTRTTTTPFPTIHLRSSPSLPPASPCPALA
FWKRVRIGLEDIWNSLSSVFTEMQPIDRNQR

TQSTT "TSTT650

FIGURE 215

CCCGGGTGACCCACGCGTCCGGGGAGAAAGG**ATG**CGCCGGCCTGGCGGCGCGGTTGGTCTGCTAGCTGGGGCA
 GCGGCGCTGGCGAGCGGCTCCCAGGGCGACCGTGAGCCGGTGTACCGCGACTGCGTACTGCAGTGCGAAGAGCA
 GAACTGCTCTGGGGGCGCTCTGAATCACTTCCGCTCCCGCCAGCCAATCTACATGAGCTAGCAGGCTGGACCT
 GTCGGGACGACTGTAAGTATGAGTGATGTGGGTCAACGTTGGGCTCTACCTCCAGGAAGGTCAAAAGTGCCT
 CAGTTCCATGGCAAGTGGCCCTTCTCCCGGTTCTGTTCTTTCAAGAGCCGGCATCGGCCGTGGCCTCGTTTCT
 CAATGGCCTGGCCAGCCTGGTGATGCTCTGCCGCTACCGCACCTTCGTGCCAGCCTCCTCCCCATGTACCACA
 CCTGTGTGGCCTTCGCTGGGTGTCCCTCAATGCATGGTTCTGGTCCACAGTCTTCCACACCAGGGACACTGAC
 CTCACAGAGAAAAATGGACTACTTCTGTGCCCTCCACTGTCATCCTACACTCAATCTACCTGTGCTGCGTCAGGAC
 CGTGGGGCTGCAGCACCCAGCTGTGGTCAGTGCCTTCCGGGCTCTCCTGCTGCTCATGCTGACCGTGCACGTCT
 CCTACCTGAGCCTCATCCGCTTCGACTATGGCTACAACCTGGTGGCCAACGTGGCTATTGGCCTGGTCAACGTG
 GTGTGGTGGCTGGCCTGGTGCCTGTGGAACCAGCGGCGGCTGCCTCACGTGCGCAAGTGCCTGGTGGTGGTCTT
 GCTGCTGCAGGGGCTGTCCCTGCTCGAGCTGCTTGACTTCCCACCGCTCTTCTGGGTCTGGATGCCCATGCCA
 TCTGGCACATCAGCACCATCCCTGTCCACGTCCTCTTTTTCAGCTTTCTGGAAGATGACAGCCTGTACCTGCTG
 AAGGAATCAGAGGACAAGTTCAAGCTGGACT**TGA**AGACCTTGGAGCGAGTCTGCCCCAGTGGGGATCCTGCCCC
 GCCCTGCTGGCCTCCCTTCTCCCTCAACCTTGAGATGATTTTCTCTTTTCAACTTCTTGAAGTGGACATGA
 AGGATGTGGGCCCAGAATCATGTGGCCAGCCACCCCTGTTGGCCCTCACCAGCCTTGGAGTCTGTTCTAGGG
 AAGGCCCTCCAGCATCTGGGACTCGAGAGTGGGCAGCCCTCTACCTCCTGGAGCTGAAGTGGGGTGGAACTGA
 GTGTGTTCTTAGCTCTACCGGGAGGACAGTGCCTGTTTCTTCCCACAGCCTCCTCCCCACATCCCCAGCTG
 CCTGGCTGGGTCTGAAGCCCTCTGTCTACCTGGGAGACCAGGGACCACAGGCCTTAGGGATACAGGGGTCCC
 CTTCTGTTACCAACCCCCACCTCCTCCAGGACACCACTAGGTGGTGTGCTGGATGCTTGTCTTTGGCCAGCCAA
 GGTTCACGGCGATTCTCCCCATGGGATCTTGAGGGACCAAGCTGCTGGGATTGGGAAGGAGTTTACCCTGACC
 GTTGCCCTAGCCAGGTTCCCAGGAGGCTCACCATACTCCCTTTCAGGGCCAGGGCTCCAGCAAGCCCAGGGCA
 AGGATCCTGTGCTGCTGTCTGGTTGAGAGCCTGCCACCGTGTGTGCGGAGTGTGGGCCAGGCTGAGTGCATAGG
 TGACAGGGCCGTGAGCATGGGCCTGGGTGTGTGTGAGCTCAGGCCTAGGTGCGCAGTGTGGAGACGGGTGTTGT
 CGGGGAAGAGGTGTGGCTTCAAAGTGTGTGTGTGAGGGGGTGGGTGTGTTAGCGTGGGTTAGGGGAACGTGTG
 TCGCGTGCTGGTGGGCATGTGAGATGAGTGACTGCCGGTGAATGTGTCCACAGTTGAGAGGTTGGAGCAGGAT
 GAGGGAATCCTGTCAACATCAATAATCACTTGTGGAGCGCCAGCTCTGCCAAGACGCCACCTGGGC3GACAGC
 CAGGAGCTCTCCATGGCCAGGCTGCCTGTGTGCATGTTCCCTGTCTGGTGCCCTTTGCCCGCTCCTGCAAAC
 CTCACAGGGTCCCCACACAACAGTGCCCTCCAGAAGCAGCCCTCGGAGGCAGAGGAAGGAAAATGGGGATGGC
 TGGGGCTCTCTCCATCCTCCTTTTCTCCTTGCCTTCGCATGGCTGGCCTTCCCCTCCAAAACCTCCATTCCCCT
 GCTGCCAGCCCCCTTTGCCATAGCCTGATTTTGGGGAGGAGGAAGGGGCGATTTGAGGGAGAAGGGGAGAAAGCT
 TATGGCTGGGTCTGGTTTCTTCCCTTCCCAGAGGGTCTTACTGTTCCAGGGTGGCCCCAGGGCAGGCAGGGGCC
 AACTATGCCTGTGCCCTGGTAAAGGTGACCCCTGCCATTTACCAGCAGCCCTGGCATGTTCTGCCCCACAGG
 AATAGAATGGAGGGAGCTCCAGAACTTTCCATCCCAAAGGCAGTCTCCGTGGTTGAAGCAGACTGGATTTTTG
 CTCTGCCCTGACCCCTTGTCCCTCTTTGAGGGAGGGGAGCTATGCTAGGACTCCAACCTCAGGGACTCGGGTG
 GCCTGCGCTAGCTTCTTTTGATACTGAAAACCTTTAAGGTGGGAGGGTGGCAAGGGATGTGCTTAATAAATCAA
 TTCCAAGCCTCAAAAAAAAAAAAAAAAAA

FIGURE 216

MAGLAARLVLLAGAAALASGSQGDREPVYRDCVLQCEEQNCSGGALNHFRSRQPIYMSLAGW
TCRDDCKYECMWVTVGLYLQEGHKVPQFHGKWPFSSRFLFFQEPASAVASFLNGLASLVMLCR
YRTFVPASSPMYHTCVAFAWVSLNAFWSTVFHTRDSDLTEKMDYFCASTVILHSIYLCCVR
TVGLQHPAVVSAFRALLLLMLTVHVSYLSLIRFDYGYNLVANVAIGLVNVVWWLAWCLWNQR
RLPHVRKCVVVVLLLQGLSLLELLDFPPLFWVLDAAHAIWHISTIPVHVLFFSFLEDDSLYLL
KESEDKEKLD

Important features:

Signal peptide:

amino acids 1-20

Transmembrane domains:

amino acids 105-123, 138-156, 169-185, 193-209, 221-240, 256-272

N-glycosylation site.

amino acids 40-44

N-myristoylation site.

amino acids 43-49

CUB domain proteins profile.

amino acids 285-302

Amiloride-sensitive sodium channels proteins.

amino acids 162-186

FIGURE 217

GGCCGCCTGGAATTGTGGGAGTTGTGTCTGCCACTCGGCTGCCGGAGGCCGAAGGTCCGTGA
CT**ATG**GCTCCCCAGAGCCTGCCTTCATCTAGGATGGCTCCTCTGGGCATGCTGCTTGGGCTG
CTGATGGCCGCCTGCTTCACCTTCTGCCTCAGTCATCAGAACCTGAAGGAGTTTGCCCTGAC
CAACCCAGAGAAGAGCAGCACCAAAGAAACGGAGAGAAAAGAAACCAAAGCCGAGGAGGAGC
TGGATGCCGAAGTCCTGGAGGTGTTCCACCCGACGCATGAGTGGCAGGCCCTTCAGCCAGGG
CAGGCTGTCCCTGCAGGATCCCACGTACGGCTGAATCTTCAGACTGGGGAAAGAGAGGCCAAA
ACTCCAATATGAGGACAAGTTCCGAAATAATTTGAAAGGCCAAAAGGCTGGATATCAACACCA
ACACCTACACATCTCAGGATCTCAAGAGTGCCTGGCAAATTTCAAGGAGGGGGCAGAGATG
GAGAGTTCAAAGGAAGACAAGGCAAGGCAGGCTGAGGTAAAGCGGCTCTTCCGCCCCATTGA
GGAAGTGAAGAAAGACTTTGATGAGCTGAATGTTGTTCATTGAGACTGACATGCAGATCATGG
TACGGCTGATCAACAAGTTCAATAGTTCCAGCTCCAGTTTGGAAGAGAAGATTGCTGCGCTC
TTTGATCTTGAATATTATGTCCATCAGATGGACAATGCGCAGGACCTGCTTTCCTTTGGTGG
TCTTCAAGTGGTGATCAATGGGCTGAACAGCACAGAGCCCCCTCGTGAAGGAGTATGCTGCGT
TTGTGCTGGGCGCTGCCTTTTCCAGCAACCCCAAGGTCCAGGTGGAGGCCATCGAAGGGGGA
GCCCTGCAGAAGCTGCTGGTCATCCTGGCCACGGAGCAGCCGCTCACTGCAAAGAAGAAGGT
CCTGTTTGCCTGTGCTCCCTGCTGCGCCACTTCCCCTATGCCCAGCGGCAGTTCCTGAAGC
TCGGGGGGGCTGCAGGTCTGAGGACCCTGGTGCAGGAGAAGGGCACGGAGGTGCTCGCCGTG
CGCGTGGTCACACTGCTCTACGACCTGGTCACGGAGAAGATGTTGCGCGAGGAGGAGGCTGA
GCTGACCCAGGAGATGTCCCCAGAGAAGCTGCAGCAGTATCGCCAGGTACACCTCCTGCCAG
GCCTGTGGGAACAGGGCTGGTGCGAGATCACGGCCCACCTCCTGGCGCTGCCCGAGCATGAT
GCCCCGTGAGAAGGTGCTGCAGACACTGGGCGTCTCCTGACCACCTGCCGGGACCGCTACCG
TCAGGACCCCCAGCTCGGCAGGACACTGGCCAGCCTGCAGGCTGAGTACCAGGTGCTGGCCA
GCCTGGAGCTGCAGGATGGTGAGGACGAGGGCTACTTCCAGGAGCTGCTGGGCTCTGTCAAC
AGCTTGCTGAAGGAGCTGAGAT**TGA**GGCCCCACACCAGGACTGGACTGGGATGCCGCTAGTGA
GGCTGAGGGGTGCCAGCGTGGGTGGGCTTCTCAGGCAGGAGGACATCTTGGCAGTGCTGGCT
TGGCCATTAAATGGAAACCTGAAGGCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AA

FIGURE 218

MAPQSLPSSRMAPLGMLLGLLMAACFTFCLSHQNLKEFALTNPESSTKETERKETKAEDEL
DAEVLEV FHP THEWQALQPGQAVPAGSHVRLNLQTGEREAKLQYEDKFRNNLKGKRLDINTN
TYTSQDLKSALAKFKEGAEMESSKEDKARQAEVKRLFRPIEELKKDFDELNVVIETDMQIMV
RLINKFNSSSSSLEEKIAALFDLEYVHQM DNAQDLLSFGGLQVVINGLNSTEPLVKEYAAF
VLGAAFSSNPVKVQVEAIEGGALQKLLVILATEQPLTAKKKVLFALCSLLRHFPYAQRQFLKL
GGLQVLR TLVQEKGTEVLAVRVVTLLYDLVTEKMF AEEEEAE LTQEMSPEKLQQYRQVHLLPG
LWEQGWCEITAHLLALPEHDAREKVLQTLGVLLTTCRDRYRQDPQLGRTLASLQAEYQVLAS
LELQDGEDEGYFQELLGSVNSLLKELR

Important features:

Signal peptide:

amino acids 1-29

Hypothetical YJL126w/YLR351c/yhcX family protein.

amino acids 364-373

N-glycosylation site.

amino acids 193-197, 236-240

N-myristoylation site.

amino acids 15-21, 19-25, 234-240, 251-257, 402-408, 451-457

Homologous region SLS1 protein.

amino acids 68-340

[illegible]

FIGURE 221

AAGCTGGTTTAAGGAAGCAGAGGAGGGTTAGATTTCGTTGAGTGAGGACGGAAGATCAACCCA
TTTCCATTCCGCCAGATGGCCTATGTTTCTGGTCTCTCCCTTCGGNATCATCAGTGGTGTNT
TNTCTGTTATCAATATTTTGGCTGATGCANTTGGGCCAGGTGTGGTTGGGATCCATGGAGAC
TCACCCTATTANTTCCTGANTTCAGCCTTTNTGACAGCAGCCATTATCCTGCTC

GACCGACCGTTTCAGATGCCCCGGTTCCAGTACGGCTTCCTGATTTTTTGGTGCTGCTGTNTCTG
TCCTTCTACAGGAGGTGTTCCGCTTTGCCTANTACAAGCTGCTTAAGAAGGCAGATGAGGGG
TTAGCATNGCTGAGTGAGGACGGAAGATCACCCATTTCCATCCGCCAGATGGCCTATGTTTN
TGGTNTTTCCTTCGGTATCATCAGTGGTGTNTTCTGTTATCAATATTTTGGNTGATGCAN
TTGGGGCCAGGTGTGGTTGGGATCCATGGAGANTCACCTATTAATTCCTGAATTCAGCCTTT
NTGACAGCAGCCATTATCCTGNTCCATACCTTTTGGGGAGTTGTGTTTTTTGATGCCTGTGA
GAGGAG

NGTTGGAGAAGTGGCGCGGACNTTCATTTGGGGTTTCGGTTCCTCCCTTTCCCTTTCCCGG
GGGTCTGGGGTGACATTGCACGGGCCCCCTCGTGGGGTCGCGTTGCCACCCACGCGGACTCC
CCAGNTGGNGCGCCCTTCCCATTTGCCTGTCCTGGTCAGGCCCCCACCCCCCTTCCCACNTG
ACCAGCCATGGGGGCTGCGGTGTTTTTCGGCTGCACTTTCGTCGCGTTCGGCCCGGCCTTCG
CGCTTTTCTTGATCACTGTGGCTGGGGACCCGCTTCGCGTTATCATCCTGGTCGCAGGGGCA
TTTTTCTGGCTGGTCTCCCTGCTCCTGGCCTCTGTGGTCTGGTTCATCTTGGTCCATGTGAC
CGACCGGTCAGATGCCCGGCTCCAGTACGGCCTCCTGATTTTTTGGTGCTGCTGTCTCTGTCC
TTCTACAGGAGGTGTTCCGCTTTGCCTACTACAAGCTGCTTAAGAAGGCAGATGAGGGGTTA
GCATCGCTGAGTGAGGACGGAAGATCACCCATCTCCATCCGCCAGATGGCCTATGTTTCTGG
TCTCTCCTTCGGTATCATCAGTGGTGTCTTCTCTGTTATCAATATTTTGGCTGATGCACTTG
GGCCAGGTGTGGTTGGGATCCATGGGAGACTCACCC

GTAAAAGAAAGTGGCCGGACCTTCATTGGGGTTCG GTTCCCCCCTTTCCCNTTCCCCGGGG
TCTGGGGGTGACATTGCACCGCGCCNCTCGTGGGGT CGCGTTGCCACCCACGCGGACTCCC
CAGNTGGCGCGCCCCCTCCCATTTGCCTGTCCTGGT CAGGCCCCCACCCTTCCCACCTGA
CCAGCCATGGGGGCTGCGGTGTTTTTCGGGCTGCACT TTCGTGCGGTTGGGGCCCGGCCTTC
GCGCTTTTCTTGATCACTGTGGCTGGGGACCCGCTT CGCGTTATCATCCTGGTGCAGGGGC
ATTTTTCTGGCTGGTCTCCCTGCTCCTGGCCTCTGT GGTCTGGTTCATCTTGGTCCATGTGA
CCGACCGGTGAGATGCCCCGGCTCCAGTACGGCCTC CTGATTTTTGGTGCTGCTGTCTCTGTC
CTTCTACAGGAGGTGTTCCGCTTTGCCTACTACAAG CTGCTTAAGAAGGCAGATGAGGGGTT
AGCATCGCTGAGTGAGGACGGAAGATCACCCATCTC CATCCGCCAGATGGCCTATGTTTCTG
GTCTCTCCTTCGGTATCATCAGTGGTGTCTTCTCT GTTATCAATATTTTGGCTGATGCACTT
GGGCCAGGTGTGGTTGGGATCCATGGAGAC

GCCCCAGGGAGCAGTGGGTGGTTATAACTCAGGCCCGGTGCCCAGAGCCCAGGAGGAGGCAG
 TGGCCAGGAAGGCACAGGCCTGAGAAGTCTGCGGCTGAGCTGGGAGCAAATCCCCACCCCC
 TACCTGGGGGACAGGGCAAGTGAGACCTGGTGAGGGTGGCTCAGCAGGCAGGGAAGGAGAGG
 TGTCTGTGCGTCCTGCACCCACATCTTTCTCTGTCCCCCTCCTTGCCCTGTCTGGAGGGCTGCT
 AGACTCCTATCTTCTGAATTCTATAGTGCCCTGGGTCTCAGCGCAGTGCCGATGGTGGCCCGT
 CCTTGTGGTTCCTCTCTACCTGGGGAAATAAGGTGCAGCGGCCATGGCTACAGCAAGACCCC
 CCTGGATGTGGGTGCTCTGTGCTCTGATCACAGCCTTGCTTCTGGGGGTACAGAGCATGTT
 CTCGCCAACAAATGATGTTTTCCTGTGACCACCCCTCTAACACCGTGCCCTCTGGGAGCAACCA
 GGACCTGGGAGCTGGGGCCGGGGAAGACGCCCGGTGCGATGACAGCAGCAGCCGCATCATCA
 ATGGATCCGACTGCGATATGCACACCCAGCCGTGGCAGGCCGCGCTGTTGCTAAGGCCCAAC
 CAGCTCTACTGCGGGGCGGTGTTGGTGCATCCACAGTGGCTGCTCACGGCCGCCCACTGCAG
 GAAGAAAGTTTTTCAGAGTCCGTCTCGGCCACTACTCCCTGTCACCAGTTTATGAATCTGGGC
 AGCAGATGTTCCAGGGGGTCAAATCCATCCCCACCCTGGCTACTCCCACCCTGGCCACTCT
 AACGACCTCATGCTCATCAAACCTGAACAGAAGAATTCGTCCCACTAAAGATGTCAGACCCAT
 CAACGTCTCCTCTCATTTGTCCCTCTGCTGGGACAAAGTGCTTGGTGTCTGGCTGGGGGACAA
 CCAAGAGCCCCCAAGTGCACTTCCCTAAGGTCCTCCAGTGCTTGAATATCAGCGTGCTAAGT
 CAGAAAAGGTGCGAGGATGCTTACCCGAGACAGATAGATGACACCATGTTCTGCGCCGGTGA
 CAAAGCAGGTAGAGACTCCTGCCAGGGTGATTCTGGGGGGCCTGTGGTCTGCAATGGCTCCC
 TGCAGGGACTCGTGCTCCTGGGGAGATTACCCTTGTGCCCGGCCCAACAGACCGGGTGTCTAC
 ACGAACCTCTGCAAGTTCACCAAGTGGATCCAGGAAACCATCCAGGCCAACTCCTGAGTCAT
 CCCAGGACTCAGCACACCGGCATCCCCACCTGCTGCAGGGACAGCCCTGACACTCCTTTTCAG
 ACCCTCATTCTTTCCCAGAGATGTTGAGAATGTTTCATCTCTCCAGCCCCTGACCCCATGTCT
 CCTGGACTCAGGGTCTGCTTCCCCCACATTGGGCTGACCGTGTCTCTCTAGTTGAACCCTGG
 GAACAATTTCCAAAACCTGTCCAGGGCGGGGGTTGCGTCTCAATCTCCCTGGGGCACTTTTCAT
 CCTCAAGCTCAGGGCCCATCCCTTCTCTGCAGCTCTGACCCAAATTTAGTCCCAGAAATAAA
 CTGAGAAGTGGAAAAAAAAAA

FIGURE 226

MATARPPWMWVLCALITALLGVTEHVLANNNDVSCDHPSNTVPSGSNQDLGAGAGEDARSDD
SSSRIINGSDCDMHTQPWQAALLLRPNQLYCGAVLVHPQWLLTAAHCRKKVFRVRLGHYSLS
PVYESGQOMFQGVKSIHPHGYSHPGHSNDLMLIKLNRRIRPTKDVRPINVSSHCP SAGTKCL
VSGWGTTKSPQVHF PKVLQCLNISVLSQKRCE DAYPRQIDDTMFCAGDKAGRDSCQGD SGGP
VVCNGSLQGLVSWGDYPCARPNRPGVYTNLCKFTKWIQETIQANS

0994131.11601

ATGGTCTCAACGACCGGTGGAAGACCATGGGCGGCGCTGCCCAACTTGAGGACCGGCCGCGCGA
CAAGCCGCAGCGGCCGAGCTGCGGCTACGTGCTGTGCACCGTGCTGCTGGCCCTGGCTGTGC
TGCTGGCTGTAGCTGTACCGGTGCCGTGCTCTTCTGTAACACAGCCACAGCGCCGGGACG
GCGCCCCACCTGTCTGCTAGCACTGGGGCTGCCAGCCCAACAGCGCCCTGGTCACTGTGGA
AAGGGCGGACAGCTCGCACCTCAGCATCTCTATTGACCCGCGCTGCCCGACCTCACCACA
GCTTCGCACGCCTGGAGAGCGCCCAGGCCTCGGTGCTGCAGGCGCTGACAGAGCACCAGGCC
CAGCCACGGCTGGTGGGCGACCAGGAGCAGGAGCTGCTGGACACGCTGGCCGACCAGCTGCC
CCGGCTGCTGGCCCCGAGCCCTCAGAGCTGCAGACGGAGTGATGGGGCTGCGGAAGGGGCATG
GCACGCTGGGCCAGGGCCTCAGCGCCCTGCAGAGTGAGCAGGGCCGCTCATCCAGCTTCTC
TCTGAGAGCCAGGGCCACATGGCTCACTGGTGAACCTCCGTACGCGACATCCTGGATGCCCT
GCAGAGGGACCGGGGGCTGGGCCGGCCCCGCAACAAGGCCGACCTTCAGAGAGCGCCTGCC
GGGGAACCCGGCCCCCGGGGCTGTGCCACTGGCTCCCGGCCCGAGACTGTCTGGACGTCCTC
CTAAGCGGACAGCAGGACGATGGCGTCTACTCTGTCTTTCCACCCACTACCCGGCCGGCTT
CCAGGTGTACTGTGACATGCGCAGGACGGCGGGCTGGACGGTGTTTACGCGCCGGGAGG
ACGGCTCCGTGAACCTTCTCCGGGGCTGGGACGCGTACCGAGACGGCTTTGCGAGGCTCACC
GGGGAGCACTGGCTAGGGCTCAAGAGGATCCACGCCCTGACCACACAGGCTGCCTACGAGCT
GCACGTGGACCTGGAGGACTTTGAGAATGGCACGGCCTATGCCCGCTACGGGAGCTTCGGCG
TGGGCTTGTTCTCCGTGGACCCTGAGGAAGACGGGTACCCGCTACCGTGGCTGACTATTCC
GGCACTGCAGGCGACTCCCTCCTGAAGCACAGCGGCATGAGGTTTACCACCAAGGACCGTGA
CAGCGACCAATTCAGAGAACAACGTGTGCCCTTCTACCGCGGTGCCCTGGTGGTACCGCAACT
GCCACACGTCCAACCTCAATGGGCAGTACCTGCGCGGTGCGCACGCCTCCTATGCCGACGGC
GTGGAGTGGTCTCCTGGACCGGCTGGCAGTACTCACTCAAGTTCTCTGAGATGAAGATCCG
GCCGGTCCGGGAGGACCGCT**TAG**ACTGGTGCACATTGTCTTTGGCCCTGCTGGTCCCTGTGCG
CCACTCCCGACCCACCTCACTCTTTCTGTAATGTTCTCCACCACCTGTGCCTGGCGGAC
CCACTCTCCAGTAGGGAGGGGCGGGCCACTCCCTGACACGAAGCTCCCTGGGCGGTGAAGT
CACACATCGCCTTCTCGCCGTCCCCACCCCTCCATTTGGCAGCTCACTGATCTCTTGCCTC
TGCTGATGGGGGCTGGCAAACCTTGACGACCCCAACTCCTGCCTGCCCCCACTGTGACTCCGG
TGCTGTTTGGCGTCCCTGGCCAGGATGGTGGAGTCTGCCCCAGGCACCTCTGCCCTGCC
GGCCAAATACCCGGCATTATGGGGACAGAGAGCAGGGGGCAGACAGCACCCTGGAGTCCCTC
CTAGCAGATCGTGGGGAATGTGAGGTCTCTCTGAGGTCAAGTCTGAGGCCAGTATCCTCCAG
CCCTCCCAATGCCAACCCCCACCCCGTTTCCCTGGTGCCAGAGAACCACCTCTCCCCAA
GGGCCTCAGCCTGGCTGTGGGCTGGGTGGCCCCATCCTACCAGGCCCTGAGGTCAAGGATGGG
GAGCTGCTGCCTTTGGGGACCCACGCTCCAAGGCTGAGACCAGTTCCTGGAGGCCACCCAC
CCTGTGCCCGGACGGCTGGGCTGTCAGTCTCTTACCTGCTGTGCCCACTGCTCTCTG
TCTCAAATGAGGGCCCAACCCATCCCCACCCAGCTCCCGGCGCTCCTCCTACCTGGGGCAGC
CGGGGCTGCCATCCCATTCTCCTGCCTCTGGAAGGTGGGTGGGGCCCTGCACCGTGGGGCT
GGACTGCGCTAATGGGAAGCTCTTGTTTTCTGGGCTGGGGCTAGGCAGGGCTGGGATGAG
GCTTTGACAAACCCACACCAATTTCCAGGGACTCCAGGGTCTTGGGCTCCTCCAGGAGG
GCCTTTGGGGTGATGACCCCTTCCCTGAGGTGGCTGTCTCATGAGGAGGCCAACCCTTGGC
ATTGACCGTGGCCACCTGGACCCAGGCCAGGCCCGGCCGCGAGTGGTCAAGGGACAGGGA
CCACCTCACCGGGCAAATGGGGTGGGGGGAGTGGGGCACCAGACCAGGCACCACCTGGACA
CTTTCTTGTTGAATCCTCCCAACACCCAGCAGCTGTATCCCCACTCCTTGTGTGCACACA
TGCAGAGTGTAGACCCCGAGGCTCCAGGACGAGCAGCCACAAGGGCAGGGCTGGAGCCGGG
TCCTCAGCTGTCTGCTCAGCAGCCCTGGACCCGCGTGCGTTACGTACGGCCAGATGACAGGG
CGGCTTTTCCAAGGCCTCCTGATGGGGGCTCCGAAAGGGCTGGAGTCAGCCTTGGGGAGCT
GCCTAGCAGCCTCTCCTCGGGCAGGAGGGGAGGTGGCTTCTTCCAAGGACACCCGATGGCA
GGTGCTTAGGGGTGTGGGGGTTCCGTTCTCCCTTCCCTCCCACTGAAGTTTGTGCTTAAAA
AACAATAAATTTGACTTGGCACCACTGGGGCTTGGGTTGGTGGGAGAGGCCGTGTGACCTGGCTCTC
TGTCCCACTGCCACCAGGTCACTCCACATGCGCAG

FIGURE 228

MVNDRWKTMGGAAQLEDPRDPKPQRPSGCVLCTVLLALAVLLAVAVTGAVLFLNHAHAPGT
APPPVVSTGAASANSALVTVERADSSHLSILIDPRCPDLTDSFARLESAQASVLQALTEHQA
QPRLVGDQEQELDLADQLPRLARASELQTECMGLRKGHGTLGQGLSALQSEQGRLIQLL
SESQGHMAHLVNSVSDILDALQDRGLGRPRNKADLQAPARGTRPRGCATGSRPRDCLDVL
LSGQQDDGVYSVFPTHYPAGFQVYCDMRTDGGGWTVFQRRDGSVNFFRGWDAYRDGFGRLT
GEHWLGLKRIHALTTQAAYELHVDLEDFENGTAARYGSFGVGLFSVDPEEDGYPLTVADYS
GTAGDSLKXSGMRFTTKDRSDHSENNCAAFYRGAWWYRNCHTSNLNGQYLGAHASADG
VEWSSWTGWQYSLKFSEMKIRPVREDR

FIGURE 229

GCAGTCAGAGACTTCCCCTGCCCCTCGCTGGGAAAGAACATTAGGAATGCCTTTTAGTGCCT
 TGCTTCCTGAACTAGCTCACAGTAGCCCGGCGGCCAGGGCAATCCGACCACATTTCACTCT
 CACCGCTGTAGGAATCCAGATGCAGGCCAAGTACAGCAGCACGAGGGACATGCTGGATGATG
 ATGGGGACACCACCATGAGCCTGCATTCTCAAGCCTCTGCCACAACCTCGGCATCCAGAGCCC
 CGGCGCACAGAGCACAGGGCTCCCTCTTCAACGTGGCGACCAGTGGCCCTGACCCTGCTGAC
 TTTGTGCTTGGTGCTGCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTTTTTTCAGTACTACC
 AGCTCTCCAATACTGGTCAAGACACCATTTCTCAAATGGAAGAAAGATTAGGAAATACGTCC
 CAAGAGTTGCAATCTCTTCAAGTCCAGAATATAAAGCTTGCAGGAAGTCTGCAGCATGTGGC
 TGAAAAACTCTGTCGTGAGCTGTATAACAAAGCTGGAGCACACAGGTGCAGCCCTTGTACAG
 AACAAATGGAATGGCATGGAGACAATTGCTACCAGTTCTATAAAGACAGCAAAAGTTGGGAG
 GACTGTAAATATTTCTGCCTTAGTGAAAACCTCTACCATGCTGAAGATAAACAAACAAGAAGA
 CCTGGAATTTGCCGCGTCTCAGAGCTACTCTGAGTTTTTCTACTCTTATTGGACAGGGCTTT
 TGCGCCCTGACAGTGGCAAGGCCTGGCTGTGGATGGATGGAACCCCTTTCATTCTGAACTG
 TTCCATATTATAATAGATGTCACCAGCCCAAGAAGCAGAGACTGTGTGGCCATCCTCAATGG
 GATGATCTTCTCAAAGGACTGCAAAGAATTGAAGCGTTGTGTCTGTGAGAGAAGGGCAGGAA
 TGGTGAAGCCAGAGAGCCTCCATGTCCCCCTGAAACATTAGGCGAAGGTGACTTGATTCGCC
 CTCTGCAACTACAAATAGCAGAGTGAGCCAGGCGGTGCCAAAGCAAGGGCTAGTTGAGACAT
 TGGGAAATGGAACATAATCAGGAAAGACTATCTCTCTGACTAGTACAAAATGGGTTCCTCGTG
 TTTCTCTGTTTCTGAGGATCACCAGCATTTCTGAGCTTGGGTTTATGCACGTATTTAACAGTCACA
 AGAAGTCTTATTTACATGCCACCAACCAACCTCAGAAACCCATAATGTCATCTGCCTTCTTG
 GCTTAGAGATAACTTTTAGCTCTCTTTCTTCTCAATGTCTAATATCACCTCCCTGTTTTTCTAT
 GTCTTCCTTACACTTGGTGGAATAAGAACTTTTTGAAGTAGAGGAAATACATTGAGGTAAC
 ATCCTTTTCTCTGACAGTCAAGTAGTCCATCAGAAATTGGCAGTCACTTCCCAGATTGTACC
 AGCAAATACACAAGGAATTCTTTTTGTTTGTTCAGTTCATACTAGTCCCTTCCCAATCCAT
 CAGTAAAGACCCCATCTGCCTTGTCCATGCCGTTTCCCAACAGGGATGTCACTTGATATGAG
 AATCTCAAATCTCAATGCCTTATAAGCATTCCTTCCTGTGTCCATTAAGACTCTGATAATTG
 TCTCCCCCTCCATAGGAATTTCTCCCAGGAAAGAAATATATCCCCATCTCCGTTTTCATATCAG
 AACTACCGTCCCCGATATTCCCTTCAGAGAGATTAAAGACCAGAAAAAGTGAGCCTCTTCA
 TCTGCACCTGTAATAGTTTTCAGTTCCTATTTTCTTCCATTGACCCATATTTATACCTTTTCTAG
 GTACTGAAGATTTAATAATAATAAATGTAAATACTGTGAAAAA

FIGURE 230

MQAKYSSTRDMLDDDGDTTMSLHSQASATTRHPEPRRTEHRAPSSTWRPVALTLLTLCLVLL
IGLAALGLLFFQYYQLSNTGQDTISQMEERLGNTSQELQSLQVQNIKLAGSLQHVAEKLCRE
LYNKAGAHRCSPCTEQWKWHGDNCYQFYKDSKSWEDCKYFCLSENSTMLKINKQEDLEFAAS
QSYSEFFYSYWTGLLRPDSGKAWLWMDGTPFTSELFHIIIDVTSPRSRDCVAILNGMIFSKD
CKELKRCVCERRAGMVKPESLHVPPETLGEGD

FIGURE 231

AATTTTCACCGCTGTAGGAATCCAGATGCAGGCCAAGTACAGCAGCACGAGGGACATGNTGG
ATGATGATGGGACACCACCATGAGCCTGCATTNTCAAGCTTTTGCCACAATTCGGCATCCAG
AGCCCCGGCGCACAGAGCACAGGGNTCCTTTTTTCAACGTGGCGACCAGTGGCCCTGACCCTG
CTGACTTTGTGCTTGGTGCTGCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTTTTTTCAGTA
CTACCAGCTCTCCAATACTGGTCAAGACACCATTCTCAAATGGAAGAAAGATTAGGAAATA
CGTCCCAAGAGTTGCAATTTNTTCAAGTCCAGAATATAAAGCTTGCAGGAAGTNTGCAGCAT
GTGGCTGAAAACTCTGTCGTGAGCTGTATAACAAAGCTGGAGGAACTTTGAAGGAGGGCAA
AGTNTCCTCATNTACTATACACACACCACTTCCC

[illegible]

FIGURE 233

MRASLLLSVLRPAGPVAVGISLGF TLSLLSVTWVEEPCGPGPPQPGDSELPPRGNTNAARRP
NSVQPGAEREKPGAGEGAGENWEPRVLPYHPAQPGQAACKAVRTRYISTELGIRQRLLVAVL
TSQTTLPTLGVAVNRTLGHRLERVVFLTGARGRRAPPGMAVVTLGEERPIGHLHLALRHLL
QHGD DFDWFFLVPDTTYTEAHGLARLTGHLSLASAAHLYLGRPQDFIGGEPTPGRYCHGGFG
VLLSRMLLQQLRPHLEGCRNDIVSARPDEWLGRCIL DATGVGCTGDHEGVHYSHLELSPGEP
VQEGDPHF RSALT AHPVRDPVHMYQLHKAFARAE LERTYQEIQELQWEIQNTSHLAVDGDRA
AAWPVGIPAPSRPASRFEVLRWDYFTEQHAFSCADGSPRCPLRGADRADVADVLGTALEELN
RRYHPALRLQKQQLVNGYRRFDPARGMEYTLDLQLEALT PQGGRRPLTRRVQLLRPLSRVEI
LPVPYVTEASRLTVLLPLAAAERDLAPGFLEAFATAALEPGDAAAALTLLLLLYEPRQAQRVA
HADVFAPVKAHVAELERRFPGARVPWLSVQTAAPSPLRLMDLLSKKHPLDTL FLLAGPDTVL
TPDFLNRCRMHAISGWQAFFPMHFQAFHPGVAPPQGP GPPELGRDTGRFDRQAASEACFYNS
DYVAARGRLAAASEQEEELLES LDVYELFLHFSSLHVLRAVEPALLQRYRAQTCSARLSEDL
YHRCLQSVLEGLGSRTQLAMLLFEQE QGNST

235/330

FIGURE 235

MAAGLFGLSARRLLAAAATRG LPAARVRWESSFSRTVVAPSAVAGKRPPEPTTPWQEDPEPE
DENLYEKNPD SHGYDKDPVLDVWNMRLVFFFGVSIILVLGSTFVAYLPDYRMKEWSRREAER
LVKYREANGLPIMESNCFDPSKIQLPEDE

FIGURE 235

FIGURE 236

GGCGGCTGGGCTGTTTGGTTTGAGCGCTCGCCGTCTTTTGGCGGCAGCGGCGACGCGAGGGC
TCCCGGCCGCCCCGCGTCCGCTGGGAATCTAGCTTCTCCAGGACTGTGGTCGCCCCGTCCGCT
GTGGCGGGAAAGCGGCCCCCAGAACCGACCACACCGTGGCAAGAGGACCCAGAACCCGAGGA
CGAAAACTTGTATGAGAAGAACCCAGACTCCCATGGTTATGACAAGGACCCCGTTTTGGACG
TCTGGAACATGCGACTTGTCTTCTTCTTTGGCGTCTCCATCATCCTGGTCCTTGGCAGCACC
TTTGTGGCCTATCTGCCTGACTACAGGATGAAAGAGTGGTCCCGCCGCGAAGCTGAGAGGCT
TGTGAAATACCGAGAGGCCAATGGCCTTCCCATCATGGAATCCAACCTGCTTCGACCCCAGCA
AGATCCAG

FIGURE 237

GCGGCGGCT**ATG**CCGCTTGCTCTGCTCGTCCTGTTGCTCCTGGGGCCCGGCGGCTGGTGCCT
 TGCAGAACCCCCACGCGACAGCCTGCGGGAGGAACCTTGTCATCACCCCGCTGCCTTCCGGGG
 ACGTAGCCGCCACATTCCAGTTCCGCACGCGCTGGGATTCGGAGCTTCAGCGGGAAGGAGTG
 TCCCATTACAGGCTCTTTCCCAAAGCCCTGGGGCAGCTGATCTCCAAGTATTCTCTACGGGA
 GCTGCACCTGTCATTACACAAGGCTTTTGGAGGACCCGATACTGGGGGCCACCCCTTCCCTGC
 AGGCCCCATCAGGTGCAGAGCTGTGGGTCTGGTTCCAAGACACTGTCACTGATGTGGATAAA
 TCTTGGAAGGAGCTCAGTAATGTCCTCTCAGGGATCTTCTGCGCCTCTCTCAACTTCATCGA
 CTCCACCAACACAGTCACTCCCCTGCTCCTTCAAACCCCTGGGTCTGGCCAATGACACTG
 ACCACTACTTTCTGCGCTATGCTGTGCTGCCGCGGGAGGTGGTCTGCACCGAAAACCTCACC
 CCCTGGAAGAAGCTCTTGCCCTGTAGTTCCAAGGCAGGCCTCTCTGTGCTGCTGAAGGCAGA
 TCGCTTGTTCCACACCAGCTACCACTCCCAGGCAGTGCATATCCGCCCTGTTTGAGAAATG
 CACGCTGTACTAGCATCTCCTGGGAGCTGAGGCAGACCCCTGTCAGTTGTATTTGATGCCTTC
 ATCACGGGGCAGGGAAAGAAAGACTGGTCCCTCTTCCGGATGTTCTCCCGAACCCCTCACGGA
 GCCCTGCCCCCTGGCTTCAGAGAGCCGAGTCTATGTGGACATCACACCTACAACCAGGACA
 ACGAGACATTAGAGGTGCACCCACCCCGACCACTACATATCAGGACGTCATCCTAGGCACT
 CGGAAGACCTATGCCATCTATGACTTGCTTGACACCGCCATGATCAACAACCTCTCGAAACCT
 CAACATCCAGCTCAAGTGGAAGAGACCCCGAGAGAATGAGGCCCGCCAGTGCCCTTCCCTGC
 ATGCCCAGCGGTACGTGAGTGGCTATGGGCTGCAGAAGGGGGAGCTGAGCACACTGCTGTAC
 AACACCCACCCATACCGGGCCTTCCCGGTGCTGCTGCTGGACACCGTACCCTGGTATCTGCG
 GCTGTATGTGCACACCCCTCACCATCACCTCCAAGGGCAAGGAGAACAACCAAGTTACATCC
 ACTACCAGCCTGCCAGGACCGGCTGCAACCCACCTCCTGGAGATGCTGATTGAGCTGCCG
 GCCAACTCAGTCACCAAGGTTTCCATCCAGTTTGAGCGGGCGCTGCTGAAGTGGACCGAGTA
 CACGCCAGATCCTAACCATGGCTTCTATGTGAGCCCATCTGTCTCAGCGCCCTTGTGCCCA
 GCATGGTAGCAGCCAAGCCAGTGGACTGGGAAGAGAGTCCCCTCTTCAACAGCCTGTTCCCA
 GTCTCTGATGGCTCTAACTACTTTGTGCGGCTCTACACGGAGCCGCTGCTGGTGAACCTGCC
 GACACCGGACTTCAGCATGCCCTACAACGTGATCTGCCTCACGTGCACTGTGGTGGCCGTGT
 GCTACGGCTCCTTCTACAATCTCCTCACCCGAACCTTCCACATCGAGGAGCCCCGCACAGGT
 GGCCTGGCCAAGCGGCTGGCCAACCTTATCCGGCGCGCCCGAGGTGTCCCCCACTCT**TGA**TT
 CTTGCCCTTTCCAGCAGCTGCAGCTGCCGTTTCTCTCTGGGGAGGGGAGCCCAAGGGCTGTT
 TCTGCCACTTGCTCTCCTCAGAGTTGGCTTTTGAACCAAAGTGCCCTGGACCAGGTCAGGGC
 CTACAGCTGTGTTGTCCAGTACAGGAGCCACGAGCCAAATGTGGCATTGGAATTTGAATTAA
 CTAGAAATTCATTTCCCTCACCTGTAGTGGCCACCTCTATATTGAGGTGCTCAATAAGCAAA
 AGTGGTCGGTGGCTGCTGTATTGGACAGCACAGAAAAAGATTTCCATCACACAGAAAGGTC
 GGCTGGCAGCACTGGCCAAGGTGATGGGCTGTGCTACACAGTGTATGTCACTGTGTAGTGGA
 TGGAGTTTACTGTTTGTGGAATAAAAACGGCTGTTTCCGTGGAAAAAAAAAAAA

FIGURE 238

MPLALLVLLLLGPGGWCLAEP PRDSLREELVITPLPSGDVAATFQFRTRWDSELQREGVSHY
RLFPKALGQLISKYSLRELHLSFTQGFWRTYWGPPFLQAPSGAELWVWFQDTVTDVDKSWK
ELSNVLSGIFCASLNFIDSTNTVTPTASFKPLGLANDTDHYFLRYAVLPREVVCTENLTPWK
KLLPCSSKAGLSVLLKADRLFHTSYHSQAVHIRPVCNRARCTSSISWELRQTL SVVFDAFITG
QGKKDWSLFRMFSRTLTEPCPLASESRVYVDITTYNQDNETLEVHPPPTTTYQDVILGTRKT
YAIYDLLDTAMINNSRNLNIQLKWKRPENEAPPVPFLHAQRYVSGYGLQKGELSTLLYNTH
PYRAFPVLLLDTPWYLRLYVHTLTITSKGKENKPSYIHYQPAQDRLQPHLLEMLIQLPANS
VTKVSIQFERALLKWTEYTPDPNHGFYVSPSVLSALVPSMVAAK PVDWEESPLFNSLFPVSD
GSNYFVRLYTEPLL VNLPTPDFSMPYNVICLTCTVVAVCYGSFYNLLTRTFHIEEPRTGGLA
KRLANLIRRARGVPPL

CAACATGGGGTCCAGCAGCTTCTTGGTCCTCATGGTGTCTCTCGTTCTTGTGACCCCTGGTG
CTGTGGAAGGAGTTAAAGAGGGTATAGAGAAAGCAGGGGTTTGCCCAGCTGACAACGTACGC
TGCTTCAAGTCCGATCCTCCCCAGTGTCACACAGACCAGGACTGTCTGGGGGAAAGGAAGTG
TTGTTACCTGCACTGTGGCTTCAAGTGTGTGATTCTGTGAAGGAAGTGGGAAGAAGGAGGAA
ACAAGGATGAAGATGTGTCAAGGCCATACCCTGAGCCAGGATGGGAGGCCAAGTGTCCAGGC
TCCTCCTCTACCAGGTGTCCTCAGAAATTGATGCTGGGTCCTTTCTACCTCTGGGGGTCACTC
TCACTTGGCACCTGCCCCTGAGGGTCCTGAGACTTGGAATATGGAAGAAGCAATACCCAACC
CCACCAAAGAAAACCTGAGCTTGAAGTCCTTTTCCCCAAAAGAGGGGAAGAGTCACAAAAAG
TCCAGACCCCAGGGACGGTACTTTCCCTCTCTACCTGGTGCTCCTCCCTAATGCTCATGAAT
GGACCCCTCATGAATGAAACAGTGCCCTTATAAGAGACCCCAAAGAGCTGCCTTGCCCTTC
TGCAATGTGTGATCACAGCTAGAAGGCACTGTCAGAGAAGAGAACTGGTCCTCACCAGATG
CTGAATCTGCTGGTGCCTTGATCTTGGACTTCCCAGCCTCTAGAACTGTAAGAAATAAATAT
TTGCTGTTTATAATCCAA

FIGURE 240

MGSSSFVLVLMVSLVLTSLVAVEGVKEGIEKAGVCPADNVRCFKSDPPQCHTDQDCLGERKCC
YLHCGFKCVIPVKELEEGGNKDEDVSRPYPEPGWEAKCPGSSSTRCPQK

Signal sequence:

amino acids 1-19

N-myristoylation sites:

amino acids 23-29, 27-33, 32-38, 102-108

WAP-type 'four-disulfide core' domain signature:

amino acids 49-63

FIGURE 241

AAACTCAGCACTTGCCGGAGTGGCTCATTTGTTAAGACAAAGGGTGTGCACTTCCTGGCCAGG
 AAACCTGAGCGGTGAGACTCCCAGCTGCCTACATCAAGGCCCCAGGACATGCAGAACCTTCC
 TCTAGAACCCGACCCACCACC**ATG**AGGTCTGCCTGTGGAGATGCAGGCACCTGAGCCAAGG
 CGTCCAGTGGTCCTTGCTTCTGGCTGTCTGGTCTTCTTTCTCTTCGCCCTTGCCCTCTTTTA
 TTAAGGAGCCTCAAACAAAGCCTTCCAGGCATCAACGCACAGAGAACATTAAAGAAAGGTCT
 CTACAGTCCCTGGCAAAGCCTAAGTCCCAGGCACCCACAAGGGCGAGGAGGACAACCATCTA
 TGCAGAGCCAGCGCCAGAGAACATGCCCTCAACACACAAACCCAGCCCCAAGGCCACACCA
 CCGGAGACAGAGGAAAGGAGGCCAACCCAGGCACCGCCGGAGGAGCAGGACAAGGTGCCCCAC
 ACAGCACAGAGGGCAGCATGGAAGAGCCCAGAAAAAGAGAAAACCATGGTGAACACACTGTC
 ACCCAGAGGGCAAGATGCAGGGATGGCCTCTGGCAGGACAGAGGCACAATCATGGAAGAGCC
 AGGACACAAAGACGACCCAAGGAAATGGGGGCCAGACCAGGAAGCTGACGGCCTCCAGGACG
 GTGTCAGAGAAGCACCAGGGCAAAGCGGCAACCACAGCCAAGACGCTCATTTCCAAAAGTCA
 GCACAGAATGCTGGCTCCACAGGAGCAGTGTCAACAAGGACGAGACAGAAAGGAGTGACCA
 CAGCAGTCATCCCACCTAAGGAGAAGAAACCTCAGGCCACCCACCCCTGCCCTTTCCAG
 AGCCCCACGACGCAGAGAAACCAAAGACTGAAGGCCGCCAACTTCAAATCTGAGCCTCGGTG
 GGATTTTGAGGAAAAATACAGCTTCGAAATAGGAGGCCTTCAGACGACTTGCCCTGACTCTG
 TGAAGATCAAAGCCTCCAAGTCGCTGTGGCTCCAGAACTCTTTCTGCCCAACCTCACTCTC
 TTCCTGGACTCCAGACACTTCAACCAGAGTGAGTGGGACCGCCTGGAACACTTTGCACCACC
 CTTTGGCTTCATGGAGCTCAACTACTCCTTGGTGCAGAAGGTCGTGACACGCTTCCCTCCAG
 TGCCCCAGCAGCAGCTGCTCCTGGCCAGCCTCCCCGCTGGGAGCCTCCGGTGCATCACCTGT
 GCCGTGGTGGGCAACGGGGGCATCCTGAACAACCTCCACATGGGCCAGGAGATAGACAGTCA
 CGACTACGTGTTCCGATTGAGCGGAGCTCTCATTAAGGCTACGAACAGGATGTGGGGACTC
 GGACATCCTTCTACGGCTTTACCGCCTTCTCCCTGACCCAGTCACTCCTTATATTGGGCAAT
 CGGGGTTTCAAGAACGTGCCTCTTGGGAAGGACGTCCGCTACTTGCACTTCCTGGAAGGCAC
 CCGGGACTATGAGTGGCTGGAAGCACTGCTTATGAATCAGACGGTGATGTCAAAAAACCTTT
 TCTGGTTTCAGGCACAGACCCCAGGAAGCTTTTCGGGAAGCCCTGCACATGGACAGGTACCTG
 TTGCTGCACCCAGACTTTCTCCGATACATGAAGAACAGGTTTCTGAGGTCTAAGACCCTGGA
 TGGTGCCCACTGGAGGATATACCGCCCCACCACTGGGGCCCTCCTGCTGCTCACTGCCCTTC
 AGCTCTGTGACCAGGTGAGTGCTTATGGCTTCATCACTGAGGGCCATGAGCGCTTTTCTGAT
 CACTACTATGATACATCATGGAAGCGGCTGATCTTTTACATAAACCATGACTTCAAGCTGGA
 GAGAGAAGTCTGGAAGCGGCTACACGATGAAGGGATAATCCGGCTGTACCAGCGTCCTGGTC
 CCGGAAC TGCCAAAGCCAAGAAC**TGAC**CGGGGGCCAGGGCTGCCATGGTCTCCTTGCTGCTC
 CAAGGCACAGGATACAGTGGGAATCTTGAGACTCTTTGGCCATTTCCCATGGCTCAGACTAA
 GCTCCAAGCCCTTCAGGAGTTCCAAGGGAACACTTGAACCATGGACAAGACTCTCTCAAGAT
 GGCAAATGGCTAATTGAGGTTCTGAAGTTCTTCAGTACATTGCTGTAGGTCTTGAGGCCAGG
 GATTTTTAATTAAATGGGGTGATGGGTGGCCAATACCACAATTCCTGCTGAAAAACACTCTT
 CCAGTCCAAAAGCTTCTTGATACAGAAAAAAGAGCCTGGATTTACAGAAACATATAGATCTG
 GTTTGAATTCCAGATCGAGTTTACAGTTGTGAAATCTTGAAGGTATTACTTAACTTCACTAC
 AGATTGTCTAGAAGACCTTTCTAGGAGTTATCTGATTCTAGAAGGGTCTATACTTGTCTTG
 TCTTTAAGCTATTTGACAACCTCTACGTGTTGTAGAAAACCTGATAATAATACAAATGATTGTT
 GTCCATGGAAAGGCAAATAAATTTTCTACAGTGAAAAA

FIGURE 242

MRSCLWRCRHLSQGVQWSLLLAVLVFFLFALPSFIKEPQTKPSRHQRTENIKERSLQSLAKP
 KSQAPTRARRTTIYAEPAPENNALNTQTQPKAHTTGDRGKEANQAPPEEQDKVPHTAQRAAW
 KSPEKEKTMVNTLSPRGQDAGMASGRTEAQSWKSQDTKTTQGNNGGQTRKLTASRTVSEKHQG
 KAATTAKTLIPKSQHRMLAPTGA VSTRTRQKGVTTAVIPPEKPKQATPPPAPFQSPTTQRN
 QRLKAANFKSEPRWDFEEKYSFEIGGLQTTCPDSVKIKASKSLWLQKLFLPNLTLFLDSRHF
 NQSEWDRLEHFAPPFGFMELNYSLVQKVVTREPPVPQQQLLLASLPAGSLRCITCAVVGNGG
 ILNNSHMGQEIDSHDYVFRLSGALIKGYEQDVGTRTSFYGFATAFSLTQSLLILGNRGFKNVP
 LGKDVRYLHFLEGTRDYEWLEALLMNQTVMSKNLFWFRHRPQEAFREALHMDRYLLLHPDFL
 RYMKNRFLRSKTLGDGAHWRIYRPTTGALLLLTALQLCDQVSAYGFITEGHERFSDHYDTSW
 KRLIFYINHDFKLEREVWKRLHDEGIIRLYQRP GPGTAKAKN

Cytoplasmic Domain:

amino acids 1-10

Type II Transmembrane Domain:

amino acids 11-35

Lumenal catalytic Domain:

amino acids 36-600

Ribonucleotide Reductase small subunit Signature:

amino acids 481-496

N-glycosylation Sites:

amino acids 300-303, 311-314, 331-334, 375-378, 460-463

FIGURE 243

CGATGCGCGGACCCGGGCACCCCCTCCTCCTGGGGCTGCTGCTGGTGCTGGGGCCTTCGCCG
GAGCAGCGAGTGGAATTGTTCTCGAGATCTGAGGATGAAGGACAAGTTTCTAAAACACCT
TACAGGCCCTCTTTATTTTAGTCCAAAGTGCAGCAAACACTTCCATAGACTTTATCACAACA
CCAGAGACTGCACCATTCTGCATACTATAAAAGATGCGCCAGGCTTCTTACCCGGCTGGCT
GTCAGTCCAGTGTGCATGGAGGATAAGTGAGCAGACCGTACAGGAGCAGCACACCAGGAGCC
ATGAGAAGTGCCTTGGAACCAACAGGGAAACAGAACTATCTTTATACACATCCCCTCATGG
ACAAGAGATTTATTTTTTGACAGACTCTTCCATAAGTCCTTTGAGTTTGTATGTTGTTG
ACAGTTTGCAGATATATATTCGATAAATCAGTGTACTTGACAGTGTTATCTGTCACTTATTT

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FIGURE 244

MRGPGHPLLLGLLLVLGPSPEQRVEIVPRDLRMKDKFLKHLTGPLYFSPKCSKHFRLYHNT
RDCTIPAYYKRCARLLTRLAVSPVCMEDK

0599164 11604
TTTTTTTTTTTT

FIGURE 245

GGGCTGGGCCCCGCCGAGCTCCAGCTGGCCGGCTTGGTCCTGCGGTCCCTTCTCTGGGAGG
CCCGACCCCGGCCGCGCCAGCCCCACC**ATG**CCACCCGCGGGGCTCCGCCGGGCCGCGCCG
CTCACCGCAATCGCTCTGTTGGTGCTGGGGGCTCCCCTGGTGCTGGCCGGCGAGGACTGCCT
GTGGTACCTGGACCGGAATGGCTCCTGGCATCCGGGGTTTAACTGCGAGTTCTTCACCTTCT
GCTGCGGGACCTGCTACCATCGGTACTGCTGCAGGGACCTGACCTTGCTTATCACCGAGAGG
CAGCAGAAGCACTGCCTGGCCTTCAGCCCCAAGACCATAGCAGGCATCGCCTCAGCTGTGAT
CCTCTTTGTTGCTGTGGTTGCCACCACCATCTGCTGCTTCCTCTGTTCCCTGTTGCTACCTGT
ACCGCCGGCGCCAGCAGCTCCAGAGCCCATTTGAAGGCCAGGAGATTCCAATGACAGGCATC
CCAGTGACAGCCAGTATACCCATACCCCCAGGACCCCAAAGCTGGCCCTGCACCCCCACAGCC
TGGCTTCATGTACCCACCTAGTGGTCCTGCTCCCCAATATCCACTCTACCCAGCTGGGCCCC
CAGTCTACAACCCTGCAGCTCCTCCTCCCTATATGCCACCACAGCCCTCTTACCCGGGAGCC
TGAAGGAACCAGCCATGTCTCTGCTGCCCTTCAGTGATGCCAACCTTGGGAGATGCCCTCAT
CCTGTACCTGCATCTGGTCCTGGGGGTGGCAGGAGTCCTCCAGCCACCAGGCCCCAGACCAA
GCCAAGCCCTGGGCCCTACTGGGGACAGAGCCCCAGGGAAGTGGAACAGGAGCTGAACTAGA
ACTATGAGGGGTTGGGGGGAGGGCTTGGAATTATGGGCTATTTTTTACTGGGGGCAAGGGAGG
GAGATGACAGCCTGGGTACAGTGCCTGTTTTCAAATAGTCCCTCTGCTCCCAAGATCCCAG
CCAGGAAGGCTGGGGCCCTACTGTTTGTCCCTCTGGGCTGGGGTGGGGGGAGGGAGGAGGT
TCCGTCAGCAGCTGGCAGTAGCCCTCCTCTCTGGCTGCCCCACTGGCCACATCTCTGGCCTG
CTAGATTAAAGCTGTAAAGACAAAA

FIGURE 246

MPPAGLRRAAPLTAIALLVLGAPLVLAGEDCLWYLDRNGSWHPGFNCEFFTFCCGTCYHRYC
CRDLTLLITERQQKHCLA FSPKTIAGIASAVILFVAVVATTICCF LCSCCYLYRRRQQQLQSP
FEGQEIPMTGIPVQPVYPYPQDPKAGPAPPQPGFMYPSPGPAPQYPLYPAGPPVYNPAAPP
YMPPQPSYPGA

Transmembrane Domains:

amino acids 10-28, 85-110

N-glycosylation Site:

amino acids 38-41

N-myristoylation Sites:

amino acids 5-10, 88-93

GGGGGAGCTAGGCCGCGCGGACAGTGGTGGTGGCGGGCGCGCAAGGGGTGAGGGCGGCCCCAGAA
CCCCAGGTAGGTAGAGCAAGAAGATGGTGTCTTCTGCCCCCTCAAATGGTCCCTTGCAACCATG
TCATTTCTACTTTCTCTCACTGTTGGCTCTCTTAACCTGTGTCCACTCCTTCATGGTGTCAGAG
CACTGAAGCATCTCCAAAACGTAGTGATGGGACACCATTTCTTTGGAATAAAATACGACTTC
CTGAGTACGTCTATCCAGTTTCATTATGATCTCTTGATCCATGCAAACCTTACCACGCTGACC
TTCTGGGGAACCCAGAAAGTAGAAATCACAGCCAGTCAGCCCCACCCAGCATCATCTCTGCA
TAGTCACCACCTGCAGATATCTAGGGCCACCCTCAGGAAGGGAGCTGGAGAGAGGCTATCGG
AAGAACCCTGCAGGTCTTGAACACCCCCCTCAGGAGCAAATTGCACTGCTGGCTCCCGAG
CCCCCTCTTGTCTGGGCTCCCGTACACAGTTGTCTATTCACTATGCTGGCAATCTTTCGGAGAG
TTTCCACGGATTTTACAAAAGCACCTACAGAACCAAGGAAGGGAACTGAGGATACTAGCAT
CAACACAATTTGAACCCACTGCAGCTAGAATGGCCTTTCCCTGCTTTGATGAACCTGCCTTC
AAAGCAAGTTTTCTCAATCAAATTAGAAGAGAGCCAAAGGCACCTAGCCATCTCCAATATGCC
ATTGGTGAAATCTGTGACTGTTGCTGAAGGACTCATAGAAGACCATTTTGTATGTCACTGTGA
AGATGAGCACCCTATCTGGTGGCCTTCATCATTTTCAGATTTTGAGTCTGTGAGCAAGATAACC
AAGAGTGGAGTCAAGGTTTCTGTTTATGCTGTGCCAGACAAGATAAATCAAGCAGATTATGC
ACTGGATGCTGCGGTGACTCTTCTAGAATTTTATGAGGATTATTTTCAGCATACCGTATCCCC
TACCCAAACAAGATCTTGCTGCTATTCCCGACTTTCAGTCTGGTGCTATGGAAAACCTGGGGA
CTGACAACATATAGAGAATCTGCTCTGTTGTTTGATGCAGAAAAGTCTTCTGCATCAAGTAA
GCTTGGCATCACAGTGACTGTGGCCCATGAACCTGGCCACCACTGGTGGTGGGAACCTGGTCA
CTATGGAATGGTGAATGATCTTTGGCTAAATGAAGGATTTGCCAAATTTATGGAGTTTGTG
TCTGTGAGTGTGACCCACTCTGAACTGAAAGTTGGAGATTATTTCTTTGGCAAATGTTTTGA
CGCAATGGAGGTAGATGCTTTAAATTCCTCACACCCTGTGTCTACACCTGTGGAAAATCCTG
CTCAGATCCGGGAGATGTTTGATGATGTTTCTTATGATAAGGGAGCTTGATTTCTGAATATG
CTAAGGGAGTATCTTAGCGCTGACGCATTTAAAAGTGGTATTGTACAGTATCTCCAGAAGCA
TAGCTATAAAAATACAAAACAGGAGACCTGTGGGATAGTATGGCAAGTATTTGCCCTACAG
ATGGTGTAAAAGGGATGGATGGCTTTTGTCTAGAAAGTCAACATTCATCTTTCCTCACAT
TGGCATCAGGAAGGGGTGGATGTGAAAACCATGATGAACACTTGGACACTGCAGAGGGGTTT
TCCCTAATAAACCATCACAGTGAGGGGGAGGAATGTACACATGAAGCAAGAGCACTACATGA
AGGGCTCTGACGGCGCGCCCGGACACTGGGTACCTGTGGCATGTTCCATTGACATTCATCCC
AGCAAAATCCAACATGCTCCATCGATTTTGTCTAAAAACAAAACAGATGTGCTCATCTCACC
AGAAGAGGTGGAATGGATCAAATTTAATGTGGGCATGAATGGCTATTACATTTGTGCAATTACG
AGGATGATGGATGGGACTCTTTGACTGGCCTTTTAAAAGGAACACACACAGCAGTCAGCAGT
AATGATCGGGCAAGTCTCATTAACAATGCATTTTCAGCTCGTCAGCATTGGGAAGCTGTCCAT
TGAAAAGGCCTTGGATTTATCCCTGTACTTGAAAACATGAAACTGAAATTTATGCCCGTGTTTT
AAGGTTTGAATGAGCTGATTTCCCTATGTATAAGTTAATGGAGAAAAGAGATGATGAATGAAGT
GAAACTCAAAATTCAGGCTTTCTCATCAGGCTGCTAAGGGACCTCATTGATAAGCAGACATG
GACAGACGAGGGCTCAGTCTCAGAGCAAATGCTGCGGAGTGAACACTACTCTCTCGCCTGTG
TGCACAACATATCAGCCGTGCGTACAGAGGGGCAGAAGGCTATTTTCAGAAAGTGGGAAGGAATCC
AATGGAAACTTGAGCCTGCCTGTCGACGTGACCTTGGCAGTGTTGCTGTGGGGGCCAGAG
CACAGAAGGCTGGGATTTTCTTTATAGTAATATCAGTTTCTTTGTCAGTACTGAGAAAA
GCCAAATTTGAATTTGCCCTCTGCAGAACCCAAAATAAGGAAAAGCTTCAATGGCTACTAGAT
GAAAGCTTTAAGGGAGATAAAAATAAAAACTCAGGAGTTTCCACAAATTTCTTACACTCATTGG
CAGGAACCCAGTAGGATACCCACTGGCCTGGCAATTTCTGAGGAAAACCTGGAACAAACTTG
TACAAAAGTTTGAACCTGGCTCATCTTCCATAGGCCACATGGTAATGGGTACAACAAATCAA
TTCTCCACAAGAACCGGCTTGAAGAGGTTAAAGGATTTCTTCAAGCTCTTTTGAAGAAAATGG
TTCTCAGCTCCGTTGTGTCCAACAGACAATTGAAACCATTGAAGAAACATCCGTTGGATGG
ATAAGAATTTTGATAAAAATCAGAGTGTGGCTGCAAAGTGAAGGCTTGAACGTATGTA
TTCTCTCCCTTGCCCGGTTCTGTATATCTCTAATCACCAACATTTTGTGAGTGTATTTTCAA
ACTAGAGATGGCTGTTTTTGGCTCCAACCTGGAGATACATTTTTTCCCTTCAACTCAATTTTTGA
CTATCCCTGTGAAAAGAAATAGCTGTTAGTTTTTATCATGAATGGGCTTTTTTATGAATGGGCTA
TCGCTACCATTGTGTTTTTGTTCATCACAGGTGTTGCCCTGCAACGTAACCCCAAGTGTGGGT
TCCCTGCCACAGAAGAATAAAGTACCTTATTCTTCTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 248

MVFLPLKWSLATMSFLLSSLLALLTVSTPSWCQSTEASPKRSDGTPFPWNKIRLPEYVIPVH
 YDLLIHANLTTLTFWGTTKVEITASQPTSTIILHSHHLQISRATLRKGAGERLSEEPLOVLE
 HPPQEQIALLAPEPLLVLGPYTVVIHYAGNLSETFHGFYKSTYRTKEGELRILASTQFEPTA
 ARMAFPCFDEPAFKASFSEIKIRREPRHLAISNMPLVKSVTVAEGLIEDHFDVTVKMSTYLVA
 FIISDFESVSKITKSGVKVSVYAVPDKINQADYALDAVTLLEFYEDYFSIPYPLPKQDLAA
 IPDFQSGAMENWGLTTYRESALLFDAEKSSASSKLGITVTVAHELAHQWFGNLVTMEWWNDL
 WLNEGFAKFMEFVSVSVTHPELKVGDYFFGKCFDAMEVDALNSSHPVSTPVENPAQIREMFD
 DVSYDKGACILNMLREYLSADAFKSGIVQYLQKHSYKNTKNEDLWDSMASICPTDGVKGMDG
 FCSRSQHSSSSSHWHQEGVDVKTMMNTWTLQRGFPLITITVRGRNVHMKQEHYMKGSDGAPD
 TGYLWHVPLTFITSKSNMVHRFLLKTKTDVLILPEEVEWIKFNVGMNGYYIVHYEDDGWDSL
 TGLLKGHTAVSSNDRASLINNAFQLVLSIGKLSIEKALDLSLYLKHETEIMPVFQGLNELIP
 MYKLMKCRDMNEVETQFKAFILRLRLDLIDKQTTWDEGSVSEQMLRSELLLLACVHNYQPCV
 QRAEGYFRKWKESNGNLSLPVDVTLAVFAVGAQSTEGWDFLYSKYQFSLSSSTEKSQIEFALC
 RTQNKEKLQWLLDESFKGDKIKTQEFQILTILGRNPVGYPLAWQFLRKNWNKLVQKFELGS
 SSIAHMVMGTTNQFSTRTRLEEVKGFFSSLKENGSQLRCVQQTIEETIEENIGWMDKNFDKIR
 VWLQSEKLERM

Signal peptide:

amino acids 1-34

N-glycosylation sites:

amino acids 70-74, 154-158, 414-418, 760-764, 901-905

Neutral zinc metallopeptidases, zinc-binding region signature:

amino acids 350-360

FIGURE 249

CAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCAC
TGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGTGTCC
GACCTACCCCGGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGGTGCCAGGA
CACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGGCTGCACGG
AGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCTCTCCCTGATC
TCCTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAACTCCCTCCCGCT
TTGGGCCCCACAGCCCCAGCAGACCCAGGATCCTTGAGGTGCCAGTCTGCTTGTCTATGG
AAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGACCACACACTGTTATGAT
GGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAGAGTCCAGGGATGCATGCC
CCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTGGGCCCCGTGGGTATGACTGAGA
ACTGCAATAGGAAAGATTTTCTGACCTGTCTCGGGGGACCACCATTTATGACACACGGAAAC
TTGGCTCAAGAACCCACTGATTGGACCACATCGAATACCGAGATGTGCGAGGTGGGGCAGGT
GTGTCAGGAGACGCTGCTGCTCATAGATGTAGGACTCACATCAACCCTGGTGGGGACAAAAG
GCTGCAGCACTGTTGGGGCTCAAATTTCCCAGAAGACCACCATCCACTCAGCCCCCTCCTGGG
GTGCTTGTGGCCTCCTATACCCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAG
CAGCGTTCTGCTGAACTCCCTCCCTCCTCAAGCTGCCCCCTGTCCCAGGAGACCGGCAGTGTC
CTACCTGTGTGCAGCCCCTTGGAACCTGTTCAAGTGGCTCCCCCGAATGACCTGCCCCAGG
GGCGCCACTCATTGTTATGATGGGTACATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAT
GAGCATTCAGGGCTGCGTGGCCCAACCTTCCAGCTTCTTGTGAACCACACCAGACAAATCG
GGATCTTCTCTGCGCGTGAGAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGT
GGGGCTGAGGGCCTGGAGTCTCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTG
GTGGGGAGTGTTTTGCCCTTCTGCTTAACTCTATTACCCCCACGATTCTTCACCGCTGCTGA
CCACCCACACTCAACCTCCCTCTGACCTCATAACCTAATGGCCTTGGACACCAGATTCTTTC
CCATTCTGTCCATGAATCATCTTCCCCACACACAATCATTATATCTACTCACCTAACAGCA
ACACTGGGGAGAGCCTGGAGCATCCGGACTTGCCCTATGGGAGAGGGGACGCTGGAGGAGTG
GCTGCATGTATCTGATAATACAGACCCTGTCCTTTCA

FIGURE 250

MSAVLLLALLGFILPLPGVQALLCQFGTVQHVWKVSDLPRQWTPKNTSCDSGLGCQDTLMLI
ESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLWAPQP
PADPGSLRCPVCLSMEGCLEGTTEEICPKGTTHCYDGLLRRLRGGGIFSNLRVQGCMPPQGCN
LLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSENTEMCEVGQVCQETL
LLIDVGLTSTLVGTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLCNSASSSSVLLN
SLPPQAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLSGGGLSTKMSIQGC
VAQPSSFLLNHTRQIGIFSAEKRDVQPPASQHEGGGAEGLESITWGVGLALAPALWWGVVC
PSC

FIGURE 251

GCGACGGGCAGGACGCCCCGTTGCGCTAGCGCGTGCTCAGGAGTTGGTGTCTGCCTGCGCT
CAGGATGAGGGGGAATCTGGCCCTGGTGGGCGTTCTAATCAGCCTGGCCTTCCTGTCACTGCTG
CCATCTGGACATCCTCAGCCGGCTGGCGATGACGCCTGCTCTGTGCAGATCCTCGTCCCTGG
CCTCAAAGGGGATGCGGGAGAGAAGGGAGACAAAGGCGCCCCCGGACGGCCTGGAAGAGTCG
GCCCCACGGGAGAAAAAGGAGACATGGGGGACAAAGGACAGAAAGGCAGTGTGGGTGTCAT
GGAAAAATTGGTCCCATTGGCTCTAAAGGTGAGAAAGGAGATTCCGGTGACATAGGACCCCC
TGGTCCTAATGGAGAACCAGGCCTCCCATGTGAGTGCAGCCAGCTGCGCAAGGCCATCGGGG
AGATGGACAACCAGGTCTCTCAGCTGACCAGCGAGCTCAAGTTCATCAAGAATGCTGTGCGC
GGTGTGCGCGAGACGGAGAGCAAGATCTACCTGCTGGTGAAGGAGGAGAAGCGCTACGCGGA
CGCCAGCTGTCTGCCAGGGCCGCGGGGGCACGCTGAGCATGCCCAAGGACGAGGCTGCCA
ATGGCCTGATGGCCGCATACCTGGCGCAAGCCGGCCTGGCCCGTGTCTTCATCGGCATCAAC
GACCTGGAGAAGGAGGGCGCCTTCGTGTACTCTGACCACTCCCCCATGCGGACCTTCAACAA
GTGGCGCAGCGGTGAGCCCAACAATGCCTACGACGAGGAGGACTGCGTGGAGATGGTGGCCT
CGGGCGGCTGGAACGACGTGGCCTGCCACACCACCATGTACTTCATGTGTGAGTTTGACAAG
GAGAACATGTGAGCCTCAGGCTGGGGCTGCCCATTGGGGGCCCCACATGTCCCTGCAGGGTT
GGCAGGGACAGAGCCCAGACCATGGTGCCAGCCAGGGAGCTGTCCCTCTGTGAAGGGTGGAG
GCTCACTGAGTAGAGGGCTGTTGTCTAAACTGAGAAAATGGCCTATGCTTAAGAGGAAAATG
AAAGTGTTCCCTGGGGTGCTGTCTCTGAAGAAGCAGAGTTTCATTACCTGTATTGTAGCCCCA
ATGTCATTATGTAATTATTACCCAGAATTGCTCTTCCATAAAGCTTGTGCCTTTGTCCAAGC
TATACAATAAAATCTTTAAGTAGTGCAGTAGTTAAGTCCAAAAAAAAAAAAAAAAAAAAA

FIGURE 252

MRGNLALVGVLISLAFLSLLPSGHPQPAGDDACSVQILVPGLKGDAGEKGDKGAPGRPGRVG
PTGEKGMGDKGQKGSVGRHGKIGPIGSKGEKGDSDIGPPGPNGEPGLPCECSQLRKAIGE
MDNQVSQLTSELKFIKNAVAGVRETESKIYLLVKEEKRYADAQLSCQGRGGTLSMPKDEAAN
GLMAAYLAQAGLARVFIGINDLEKEGAFVYSDHSPMRTFNKWRSGEPNNAYDEEDCVEMVAS
GGWNDVACHTTMYFMCEFDKENM

1.031.1.131.650

FIGURE 253

AGTGACTGCAGCCTTCCTAGATCCCCTCCACTCGGTTTCTCTCTTTGCAGGAGCACCGGCAG
CACCAGTGTGTGAGGGGAGCAGGCAGCGGTCCTAGCCAGTTCCTTGATCCTGCCAGACCACC
CAGCCCCCGGCACAGAGCTGCTCCACAGGCACC**ATG**AGGATCATGCTGCTATTACAGCCAT
CCTGGCCTTCAGCCTAGCTCAGAGCTTTGGGGCTGTCTGTAAGGAGCCACAGGAGGAGGTGG
TTCCTGGCGGGGGCCGCAGCAAGAGGGATCCAGATCTCTACCAGCTGCTCCAGAGACTCTTC
AAAAGCCACTCATCTCTGGAGGGATTGCTCAAAGCCCTGAGCCAGGCTAGCACAGATCCTAA
GGAATCAACATCTCCCGAGAAACGTGACATGCATGACTTCTTTGTGGGACTTATGGGCAAGA
GGAGCGTCCAGCCAGAGGGAAAGACAGGACCTTTCTTACCTTCAGTGAGGGTTCCTCGGCCC
CTTCATCCCAATCAGCTTGGATCCACAGGAAAGTCTTCCCTGGGAACAGAGGAGCAGAGACC
TTT**TAA**GACTCTCCTACGGATGTGAATCAAGAGAACGTCCCCAGCTTTGGCATCCTCAAGT
ATCCCCCGAGAGCAGAATAGGTACTCCACTTCCGGACTCCTGGACTGCATTAGGAAGACCTC
TTTCCCTGTCCCAATCCCCAGGTGCGCACGCTCCTGTTACCCTTTCTCTCCCTGTTCTTGT
AACATTCTTGTGCTTTGACTCCTTCTCCATCTTTTCTACCTGACCCTGGTGTGGAAACTGCA
TAGTGAATATCCCCAACCCCAATGGGCATTGACTGTAGAATACCCTAGAGTTCCTGTAGTGT
CCTACATTAAAAATATAATGTCTCTCTCTATTCCCTCAACAATAAAGGATTTTTGCATATGAA
AA

FIGURE 254

MRIMLLFTAILAFSLAQSFQAVCKEPQEEVVPGGGRSKRDPDLYQLLQRLFKSHSSLEGLLK
ALSQASTDPKESTSPEKRDMDHDFVGLMGKRSVQPEGKTGPFLPSVRVPRPLHPNQLGSTGK
SSLGTEEQRPL

Important features:

Signal peptide:

amino acids 1-18

Tyrosine kinase phosphorylation site.

amino acids 36-45

N-myristoylation site.

amino acids 33-39, 59-65

Amidation site.

amino acids 90-94

Leucine zipper pattern.

amino acids 43-65

Tachykinin family signature.

amino acids 86-92

GGGCGTCTCCGGCTGCTCCTATTGAGCTGTCTGCTCGCTGTGCCCGCTGTGCCTGCTGTGCC
CGCGCTGTGCGCCGCTGCTACCGCGTCTGCTGGACGCGGGAGACGCCAGCGAGCTGGTGATTG
GAGCCCTGCGGAGAGCTCAAGCGCCCAGCTCTGCCCCAGGAGCCCAGGCTGCCCCGTGAGTC
CCATAGTTGCTGCAGGAGTGGAGCC**ATG**AGCTGCGTCCTGGGTGGTGTTCATCCCCCTTGGGGC
TGCTGTTCCCTGGTCTGCGGATCCCAAGGCTACCTCCTGCCAACGTCACCTCTCTTAGAGGAG
CTGCTCAGCAAATACCAGCACAAAGAGTCTCACTCCCGGGTCCGCAGAGCCATCCCCAGGGA
GGACAAGGAGGAGATCCTCATGCTGCACAACAAGCTTCGGGGCCAGGTGCAGCCTCAGGCCT
CCAACATGGAGTACATGGTGAGCGCCGGCTCCGGCCGCAGAGGCTGGCACCGGGGGTGGGGC
CTGGGGCCACCAGCCTGCTCTGTTCCCCAGCCAGCTCTGTTCCCCAGCCAGTGCGTGTGATGG
CTGGCTCAGGGTCTCCTCTGGCAGGGGAGGATCCCGGCTCTGTTCTGTTTTGTTTGTGTTGTT
TTGAGACAGGGTCTCACTCTGCCACTGACGCTGGAGTGCAATGGCACAATCGTCATGCCCTG
AAACCT**TAG**ACTCCCGGGGTAAAGCGATCCTGCTTCAGCCTCCCAAGTAGCTGGAACCTACAG
GCATGCACCATGGTGCCCAGCTAGATTTTAAATATTTTGTGGAGATGGGGGTCTTGCTACGT
TGCCCAGGCTGGTCTTGAACCTCCTAGGCTCAAGCAATCCTCCTGCCTCAGCCTCTCAAAGTG
CTAGGATTATAGGCATGAGTCACCCTGTCTGGCTCTGGCTCTGTTCTTAACATTCTGCCAAA
ACAACACACGTGGGTTCCTGTGCAGAGCCTGCCTCGTTGCCTTCATGTCACTCTTGGTAGC
TCCACTGGGAACACAGCTCTCAGCCTTTCCACCTGGAGGCAGAGTGGGGAGGGGGCCCAGGG
CTGGGCTTTGCTGATGCTGATCTCAGCTGTGCCACACGCTAGCTGCACCACCCTGACTTCTC
CTTAGCCCGTGTGAGCCTCACTTTCCACTTGGAGAGTCCTTCCTCGCGTGGTTGCCATGACT
GTGAGATAAGTCGAGGCTGTGAAGGGCCCGGCACAGACTGACCTGCCTCCCCAACCCCTAGG
CTTTGCTAACCGGGAAAGGAGCTAACGGTGACAGAAGACAGCCAAGGTCAACCCTCCCGGGT
GATTGTGATGGGTGTTCCAGGTGTGGTTGGGCGATGCTGCTACTTGACCCCAAGCTCCAGTG
TGGAACCTTCCTTCCTGGCTGGTTTTCCAGAACTACAGAGGAATGGACCACAGTCTTCCAGG
GTCCCTCCTCGTCCACCAACCGGGAGCCTCCACCTTGGCCATCCGTCAGCTATGAATGGCTT
TTTAAACAAACCCACGTCCCAGCCTGGGTAAACATGGTAAAGCCCCGTCTCTACAAAAAAATC
CAAGTTAGCCGGGCATGGTGGTGCGCACCTGTAGTCCCAGCTGCAGTGGGACTGAGGTGGAG
GTGGAGGTGGGGGGTGGGAGCTGAGGAAGGAGGATCGCTTGAGCCTGGGAAGTCGAGGCTGC
AGTGAGCTGAGATTGCACCACTGCACTCCAGCCTGGGTGACAGAGCAAGACCCTGTCTCAAAAA

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FIGURE 256

MSCVLGGVIPLGLLFLVCGSQGYLLPNVTLLEELLSKYQHNEHSRVRRRAIPREDKEEILML
HNKLRGQVQPQASNMEYMVSAAGSGRRGWHRGWGLGHQPALFPSQLCSPASACDGWLRVSSGR
GGSRLCSVLFVCFETGSHSATDAGVQWHNRHALKP

Important features:

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 27-31, 41-45

N-myristoylation site.

amino acids 126-132, 140-146

Amidation site.

amino acids 85-89

FIGURE 256

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FIGURE 257

AAGGAGAGGCCACCGGGACTTCAGTGTCTCCTCCATCCCAGGAGCGCAGTGGCCACT**ATG**GG
GTCTGGGCTGCCCCCTTGTCTCCTCTTGACCCTCCTTGGCAGCTCACATGGAACAGGGCCGG
GTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCCTATGAGTCCAGC
TTCCTGGAATTGCTTGAAAAGCTCTGCCTCCTCCTCCATCTCCCTTCAGGGACCAGCGTCAC
CCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACA**TGA**CAGCCATTGAAGCCTG
TGTCTTCTTGGCCCCGGGCTTTTGGGCCGGGGATGCAGGAGGCAGGCCCCGACCCTGTCTTT
CAGCAGGCCCCCACCCTCCTGAGTGGCAATAAATAAAATTTCGGTATGCTG

1.031.1.31.6.6.0

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FIGURE 258

MSGGLPLVLLLTLLGSSHGTGPGMTLQLKLKESFLTNSSYESSFELLEKLCLLLHLPSTGTS
VTLHHARSQHHVVCNT

09911-1161
T09T-13T660

FIGURE 259

AATTGTATCTGTGTAATGTTAAAACAAACGAAATAAAATAGAAGGAAAACTTTCTGAGTTT
CAAAAACAACAGACTAGTACTCTAAAGAACTCTTTAAAACAATTAAGTGTAGGATTGCAGT
TATGATTGGATATTATTTAATTCTGTTTCTGATGTGGGGTTCCTCCACTGTGTTCTGTGTGC
TATTAATATTTACCATTGCAGAAGCTTCATTCAGTGTTGAAAATGAATGCTTAGTGGATCTG
TGCCTCTTACGCATATGTTACAAATTATCTGGAGTTCCTAATCAATGCAGAGTTCCTCTCC
CTCCGATTGTTCTAAAT**TAA**TTGAAAGATGTCTGCTGTGGAAAAGGCATGTATTTAAATCTG
TATGATTCTCAACCATCTTTAGTTGGGAAAGGTCCTTGAAAGCCAATGGAAATACTTTTTTT
TTTTCTTGGCACTAATCAAGTGAGTGTTACCTTTTCACTTAGTAGGATGTGTTGTTACGCTA
GTAAAATAGAAACCTGTGTTTATTCTCAGGTATTTTAGAAACAACAGCCATCATTTTATTTT
ATGTGTGTGTTCTTGGCTGTATTCATAAATTATATATTTTGGGCTATCAAATATTACTTCAT
TCAATATAAATAACAATAGTAGAAGTTGTTTACTTAGATATGCTTTCTAGTTGCATTTTCTC
AGCCTATGTAAGACTACTTTGTTGTAATAGCCTTTGAAATTTACAGTACTGTCTCTCTACTA
TCTTCAGATTACTTGATTCAAATAAACCAATTATGTTTGTAATTGATATTAATAAAACCAGA
ATAAAAGTTCATATCTACCC

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FIGURE 260

MIGYYLILFLMWGSSTVFCVLLIFTIAEASFVENECLVDLCLLRICYKLSGVPNQCRVPLP
SDCSK

Important features:

Signal peptide:

amino acids 1-29

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FIGURE 261

GAGGATTTGCCACAGCAGCGGATAGAGCAGGAGAGCACCACCGGAGCCCTTGAGACATCCTT
 GAGAAGAGCCACAGCATAAGAGACTGCCCTGCTTGTTGTTTTGCAGG**ATG**ATGGTGGCCCTT
 CGAGGAGCTTCTGCATTGCTGGTTCTGTTCCCTTGACGCTTTTCTGCCCCCGCCGAGTGTAC
 CCAGGACCCAGCCATGGTGCATTACATCTACCAGCGCTTTCGAGTCTTGGAGCAAGGGCTGG
 AAAAATGTACCCAAGCAACGAGGGCATAACATTCAAGAATTCCAAGAGTTCTCAAAAAATATA
 TCTGTCTATGCTGGGAAGATGTCAGACCTACACAAGTGAAGTACAAGAGTGCAGTGGGTAACCTT
 GGCACTGAGAGTTGAACGTGCCCAACGGGAGATTGACTACATAACAATACCTTCGAGAGGGCTG
 ACGAGTGCATCGTATCAGAGGACAAGACACTGGCAGAAATGTTGCTCCAAGAAGCTGAAGAA
 GAGAAAAAGATCCGGACTCTGCTGAATGCAAGCTGTGACAACATGCTGATGGGCATAAAGTC
 TTTGAAAATAGTGAAGAAGATGATGGACACACATGGCTCTTGGATGAAAGATGCTGTCTATA
 ACTCTCCAAAGGTGTACTTATTAATTGGATCCAGAAACAACACTGTTTGGGAATTTGCAAAC
 ATACGGGCATTTCATGGAGGATAACACCAAGCCAGCTCCCCGGAAGCAAATCCTAACACTTTC
 CTGGCAGGGAACAGGCCAAGTGATCTACAAAGGTTTTCTATTTTTTCATAACCAAGCAACTT
 CTAATGAGATAATCAAATATAACCTGCAGAAGAGGACTGTGGAAGATCGAATGCTGCTCCCA
 GGAGGGGTAGGCCGAGCATTGGTTTACCAGCACTCCCCCTCAACTTACATTGACCTGGCTGT
 GGATGAGCATGGGCTCTGGGCCATCCACTCTGGGCCAGGCACCCATAGCCATTTGGTTCTCA
 CAAAGATTGAGCCGGGCACACTGGGAGTGGAGCATTTCATGGGATACCCCATGCAGAAGCCAG
 GATGCTGAAGCCTCATTCCTCTTGTGTGGGGTTCTCTATGTGGTCTACAGTACTGGGGGCCA
 GGGCCCTCATCGCATCACCTGCATCTATGATCCACTGGGCACTATCAGTGAGGAGGACTTGC
 CCAACTTGTCTTCCCCAAGAGACCAAGAAGTCACTCCATGATCCATTACAACCCAGAGAT
 AAGCAGCTCTATGCCTGGAATGAAGGAAACCAGATCATTTACAAACTCCAGACAAAGAGAAA
 GCTGCCTCTGAAG**TAA**TGCATTACAGCTGTGAGAAAGAGCACTGTGGCTTTGGCAGCTGTTT
 TACAGGACAGTGAGGCTATAGCCCCCTTCACAAATATAGTATCCCTCTAATCACACACAGGAAG
 AGTGTGTAGAAGTGGAATACGTATGCCTCCTTTCCCAAATGTCACTGCCTTAGGTATCTTC
 CAAGAGCTTAGATGAGAGCATATCATCAGGAAGTTTCAACAATGTCCATTACTCCCCCAA
 CCTCCTGGCTCTCAAGGATGACCACATTCTGATACAGCCTACTTCAAGCCTTTTGTCTTACT
 GCTCCCCAGCATTTACTGTAACTCTGCCATCTTCCCTCCCACAATTAGAGTTGTATGCCAGC
 CCCTAATATTCACCACTGGCTTTTCTCTCCCTGGCCTTTGCTGAAGCTCTTCCCTCTTTTT
 CAAATGTCTATTGATATTCTCCATTTTCACTGCCCAACTAAAATACTATTAATATTTCTTT
 CTTTTCTTTTCTTTTTTTTTGAGACAAGGTCTCACTATGTTGCCAGGCTGGTCTCAAACCTCC
 AGAGCTCAAGAGATCCTCCTGCCTCAGCCTCCTAAGTACCTGGGATTACAGGCATGTGCCAC
 CACACCTGGCTTAAAATACTATTTCTTATTGAGGTTTAACCTCTATTTCCCCTAGCCCTGTC
 CTTCCACTAAGCTTGGTAGATGTAATAATAAAGTGAAAATATTAACATTTGAATATCGCTTT
 CCAGGTGTGGAGTGTTCACATCATTGAATTCTCGTTTACCTTTGTGAAACATGCACAAG
 TCTTTACAGCTGTCACTTAGAGTTTAGGTGAGTAACACAATTACAAAGTGAAAGATACAGC
 TAGAAAATACTACAAATCCCATAGTTTTTCCATTGCCCAAGGAAGCATCAAATACGTATGTT
 TGTTACCTACTCTTATAGTCAATGCGTTTCATCGTTTCAGCCTAAAAATAATAGTCTGTCCC
 TTTAGCCAGTTTTTCATGTCTGCACAAGACCTTCAATAGGCCTTTCAAATGATAATTCTCTCC
 AGAAAACCAGTCTAAGGGTGAGGACCCCAACTCTAGCCTCCTCTTGTCTTGCTGTCTCTGT
 TTCTCTCTTTCTGCTTTAAATTCAATAAAAGTGACACTGAGCAAAAAAAAAAAAAA

MMVALRGASALLVLFLAAFLPPPQCTQDPAMVHYIYQRFVLEQGLEKCTQATRAYIQEFQE
FSKNISVMLGRCQTYTSEYKSAVGNLALRVERAQREIDYIQYLREADECIVSEDKTLAEMLL
QEAEKKIRTLNLASCDNMLMGIKSLKIVKKMMDTHGSMKDAVYNSPKVYLLIGSRNNTV
WEFANIRAFMEDNTKPAPRKQILTLWSQGTGQVIYKGFLEFFHNQATSNEIIKYNLQKRTVED
RMLLPGGVGRALVYQHSPSTYIDLAVDEHGLWAIHSGPGTHSHLVLTKEPRTLGEHSWDT
PCRSQDAEASFLLCGVLYVVYSTGGQGPHRITCIYDPLGTISEEDLPNLFFPKRPRSHSMIH
YNPRDKQLYAWNEGNQIIYKLQTKRKLPLK

FIGURE 263

GGGCGCCCGCGTACTCACTAGCTGAGGTGGCAGTGGTTCCACCAAC**ATG**GAGCTCTCGCAGA
 TGTGCGGAGCTCATGGGGCTGTCGGTGTTGCTTGGGCTGCTGGCCCTGATGGCGACGGCGGCG
 GTAGCGCGGGGGTGGCTGCGCGCGGGGGAGGAGAGGAGCGGCCGGCCCGCCTGCCAAAAAGC
 AAATGGATTTCACCTGACAAATCTTCGGGATCCAAGAAGCAGAAACAATATCAGCGGATTTC
 GGAAGGAGAAGCCTCAACAACACAACCTTCACCCACCGCCTCCTGGCTGCAGCTCTGAAGAGC
 CACAGCGGGAACATATCTTGATGGACTTTAGCAGCAATGGCAAATACCTGGCTACCTGTGC
 AGATGATCGCACCATCCGCATCTGGAGCACCAAGGACTTCCTGCAGCGAGAGCACCGCAGCA
 TGAGAGCCAACGTGGAGCTGGACCACGCCACCCTGGTGCCTTCAGCCCTGACTGCAGAGCC
 TTCATCGTCTGGCTGGCCAACGGGGACACCCTCCGTGTCTTCAAGATGACCAAGCGGGAGGA
 TGGGGGCTACACCTTCACAGCCACCCCAGAGGACTTCCTAAAAAGCACAAGGCGCCTGTCA
 TCGACATTGGCATTGCTAACACAGGGAAGTTTATCATGACTGCCTCCAGTGACACCACTGTC
 CTCATCTGGAGCCTGAAGGGTCAAGTGCTGTCTACCATCAACACCAACCAGATGAACAACAC
 ACACGCTGCTGTATCTCCCTGTGGCAGATTTGTAGCCTCGTGTGGCTTCACCCCAGATGTGA
 AGGTTTGGGAAGTCTGCTTTGGAAAGAAGGGGGAGTTCCAGGAGGTGGTGCAGCCCTTCGAA
 CTAAAGGGCCACTCCGCGGCTGTGCACTCGTTTGGCTTTCTCCAACGACTCACGGAGGATGGC
 TTCTGTCTCCAAGGATGGTACATGGAACTGTGGGACACAGATGTGGAATACAAGAAGAAGC
 AGGACCCCTACTTGCTGAAGACAGGCCGCTTTGAAGAGGCGGCGGGTGCCGCGCCGTGCCGC
 CTGGCCCTCTCCCCAACGCCAGGTCTTGGCCTTGGCCAGTGGCAGTAGTATTCATCTCTA
 CAATACCCGGCGGGGCGAGAAGGAGGAGTGCTTTGAGCGGGTCCATGGCGAGTGTATCGCCA
 ACTTGTCCTTTGACATCACTGGCCGCTTTCTGGCCTCCTGTGGGGACCGGGCGGTGCGGCTG
 TTTCACAACACTCCTGGCCACCGAGCCATGGTGGAGGAGATGCAGGGCCACCTGAAGCGGGC
 CTCCAACGAGAGACCCGCCAGAGGCTGCAGCAGCAGCTGACCCAGGCCCAAGAGACCCTGA
 AGAGCCTGGGTGCCCTGAAGAAG**TGAC**CTCTGGGAGGGCCCGGCGCAGAGGATTGAGGAGGAG
 GGATCTGGCCTCCTCATGGCACTGCTGCCATCTTTCCTCCCAGGTGGAAGCCTTTCAGAAGG
 AGTCTCCTGGTTTTCTTACTGGTGGCCCTGCTTCTTCCCATTTGAACTACTCTTGTCTACTT
 AGGTCTCTCTCTTCTTGCTGGCTGTGACTCCTCCCTGACTAGTGGCCAAGGTGCTTTTCTTC
 CTCCCAGGCCAGTGGGTGGAATCTGTCCCCACCTGGCACTGAGGAGAATGGTAGAGAGGAG
 AGGAGAGAGAGAGAGAATGTGATTTTTTGGCCTTGTGGCAGCACATCCTCACACCCAAAGAAG
 TTTGTAAATGTTCCAGAACAACCTAGAGAACACCTGAGTACTAAGCAGCAGTTTTGCAAGGA
 TGGGAGACTGGGATAGCTTCCCATCACAGAACTGTGTTCCATCAAAAAGACACTAAGGGATT
 TCCTTCTGGGCCTCAGTTCTATTTGTAAGATGGAGAATAATCCTCTCTGTGAACCTTTGCA
 AAGATGATATGAGGCTAAGAGAATATCAAGTCCCCAGGTCTGGAAGAAAAGTAGAAAAGAGT
 AGTACTATTGTCCAATGTCATGAAAGTGGTAAAAGTGGGAACCAAGTGTGCTTTGAAACCAA
 TTAGAAACACATTCTTGGGAAGGCAAAGTTTTCTGGGACTTGATCATACATTTTATATGGT
 TGGGACTTCTCTCTTCGGGAGATGATATCTTGTTTAAGGAGACCTCTTTTCAGTTCATCAAG
 TTCATCAGATATTTGAGTGCCCACTCTGTGCCCAAATAAATATGAGCTGGGGATTAAAAAAA
 AA

FIGURE 264

MELSQMSELMGLSVLLGLLALMATAAVARGWLRAGEERSGRPACQKANGFPPDKSSGSKKQK
QYQIRIRKEKPQQHNFTHRLLAAALKSHSGNISCMDFSSNGKYLATCADDRTIRIWKDFLQ
REHRSMRANVELDHATLVRFSPDCRAFIVWLANGDTLRVFKMTKREDGGYTFTATPEDFPKK
HKAPVIDIGIANTGKFIMTASSDTTVLIWLSLKGQVLSTINTNQMNNTAAVSPCGRFVASC
FTPDVKVWEVCFGKKGEFQEVVRAFELKGHSAVHSFAFSNDSRRMASVSKDGTWKLWDTDV
EYKKKQDPYLLKTGRFEEAAGAAPCRLALSPNAQVLALASGSSIHLYNTRRGEKEECFERVH
GECIANLSFDITGRFLASCGDRAVRLFHNTPGHRAMVEEMQGHKLRASNESTRQRLQQQLTQ
AQETLKSLGALKK

Important features:**Signal peptide:**

amino acids 1-25

N-glycosylation site.

amino acids 76-80, 92-96, 231-235, 289-293, 378-382, 421-425

Beta-transducin family Trp-Asp repeat protein.

amino acids 30-47, 105-118, 107-119, 203-216, 205-217, 296-308

FIGURE 265

TGGCCTCCCCAGCTTGCCAGGCACAAGGCTGAGCGGGAGGAAGCGAGAGGCATCTAAGCAGG
CAGTGTTTTGCCTTCACCCCAAGTGACCATGAGAGGTGCCACGCGAGTCTCAATCATGCTCC
TCCTAGTAACTGTGTCTGACTGTGCTGTGATCACAGGGGCCTGTGAGCGGGATGTCCAGTGT
GGGGCAGGCACCTGCTGTGCCATCAGCCTGTGGCTTCGAGGGCTGCGGATGTGCACCCCGCT
GGGGCGGGAAGGCGAGGAGTGCCACCCCGGCAGCCACAAGGTCCCCTTCTTCAGGAAACGCA
AGCACCACACCTGTCCTTGCTTGCCCAACCTGCTGTGCTCCAGGTTCCCGGACGGCAGGTAC
CGCTGCTCCATGGACTTGAAGAACATCAATTTTTTAGGGCGCTTGCCTGGTCTCAGGATACCCA
CCATCCTTTTCTGAGCACAGCCTGGATTTTTTATTTCTGCCATGAAACCCAGCTCCCATGAC
TCTCCCAGTCCCTACACTGACTACCCTGATCTCTCTTGTCTAGTACGCACATATGCACACAG
GCAGACATACCTCCCATCATGACATGGTCCCCAGGCTGGCCTGAGGATGTCACAGCTTGAGG
CTGTGGTGTGAAAGGTGGCCAGCCTGGTTCTCTTCCCTGCTCAGGCTGCCAGAGAGGTGGTA
AATGGCAGAAAGGACATTCCCCCTCCCCCTCCCCAGGTGACCTGCTCTCTTTCCTGGGCCCTG
CCCCTCTCCCCACATGTATCCCTCGGTCTGAATTAGACATTCTTGGGCACAGGCTCTTGGGT
GCATTGCTCAGAGTCCCAGGTCCTGGCCTGACCCTCAGGCCCTTCACGTGAGGTCTGTGAGG
ACCAATTTGTGGGTAGTTCATCTTCCCTCGATTGGTTAACTCCTTAGTTTCAGACCACAGAC
TCAAGATTGGCTCTTCCCAGAGGGGCAGCAGACAGTCACCCCAAGGCAGGTGTAGGGAGCCCA
GGGAGGCCAATCAGCCCCCTGAAGACTCTGGTCCCAGTCAGCCTGTGGCTTGTGGCCTGTGA
CCTGTGACCTTCTGCCAGAATTGTCATGCCTCTGAGGCCCCCTCTTACCACACTTTACCAGT
TAACCACTGAAGCCCCCAATTCCCACAGCTTTTCCATTAAAATGCAAATGGTGGTGGTTCAA
TCTAATCTGATATTGACATATTAGAAGGCAATTAGGGTGTTCCTTAAACAACCTCCTTTCCA
AGGATCAGCCCTGAGAGCAGGTTGGTGACTTTGAGGAGGGCAGTCCTCTGTCCAGATTGGGG
TGGGAGCAAGGGACAGGGAGCAGGGCAGGGGCTGAAAGGGGCACTGATTACAGACCAGGGAGG
CAACTACACACCAACATGCTGGCTTTAGAATAAAAGCACCAACTGAAAAAA

MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCAI SLWLRGLRMCTPLGREGE ECHP
GSHKVPFFRKRKHHTCPCLPNLLCSRFPDGRYRCSMDLKNINF

amino acids 1-19

amino acids 88-95

amino acids 33-39, 35-41, 46-52

AGCGCCCCGGGCGTCGGGGCGGTTAAAGGCCGCGCAGAAAGGGAGGCACCTTGAGAAATGTTCTTTC
CTCCAGGACCCAAGTTTCTTCACCATGGGGATGTGGTCCATTGGTGCAGGAGCCCTGGGGGC
TGCTGCCTTGGCATTGCTGCTTGCCAACACAGACGTGTTTCTGTCCAAGCCCCAGAAAGCGG
CCCTGGAGTACCTGGAGGATATAGACCTGAAAACACTGGAGAAGGAACCAAGGACTTTCAA
GCAAAGGAGCTATGGGAAAAAAATGGAGCTGTGATTATGGCCGTGCGGAGGCCAGGCTGTTT
CCTCTGTGCGAGAGGAAGCTGCGGATCTGTCTCCTCCCTGAAAAGCATGTTGGACCAGCTGGGCG
TCCCCCTCTATGCAGTGGTAAAGGAGCACATCAGGACTGAAGTGAAGGATTTCCAGCCTTAT
TTCAAAGGAGAAATCTTCTGGATGAAAAGAAAAAGTTCTATGGTCCACAAAGCGGAAGAT
GATGTTTATGGGATTTATCCGTCTGGGAGTGTGGTACAACTTCTTCCGAGCCTGGAACGGAG
GCTTCTCTGGAAACCTGGAAGGAGAAGGCTTCATCCTTGGGGGAGTTTTCGTGGTGGGATCA
GGAAAGCAGGGCATTCTTCTTGAGCACCGAGAAAAAGAATTTGGAGACAAAGTAAACCTACT
TTCTGTTCTGGAAGCTGCTAAGATGATCAAACCACAGACTTTGGCCTCAGAGAAAAAATGAT
TGTGTGAAACTGCCAGCTCAGGGATAACCAGGGACATTCACCTGTGTTTATGGGATGTATT
GTTTCCACTCGTGTCCCTAAGGAGTGAGAAACCATTTATACTCTACTCTCAGTATGGATTA
TTAATGTATTTTAATATTCTGTTTAGGCCCACTAAGGCAAAATAGCCCCAAAACAAGACTGA
CAAAAATCTGAAAAACTAATGAGGATTATTAAGCTAAAACCTGGGAAATAGGAGGCTTAAAA
TTGACTGCCAGGCTGGGTGCAGTGGCTCACACCTGTAATCCCAGCACTTTGGGAGGCCAAGG
TGAGCAAGTCACTTGAGGTCGGGAGTTCGAGACCAGCCTGAGCAACATGGCGAAACCCCGTC
TCTACTAAAAATACAAAAATCACCCGGGTGTGGTGGCAGGCACCTGTAGTCCCAGCTACCCG
GGAGGCTGAGGCAGGAGAATCACTTGAACCTGGGAGGTGGAGGTTGCGGTGAGCTGAGATCA
CACCCTGTATTCCAGCCTGGGTGACTGAGACTCTAACTAA

FIGURE 268

MSFLQDPSFFTGMWSIGAGALGAAALALLLANTDVFLSKPQKAALEYLEDIDLKTLEKEPR
TFKAKELWEKNGAVIMAVRRPGCFLCREEAADLSSLKSMLDQLGVPLYAVVKEHIRTEVKDF
QPYFKGEIFLDEKKKFYGPQRRKMMFMGFIRLGWYNFFRAWNGGFSGNLEGEFGLGGVVFV
VGSGKQGILLEHREKEFGDKVNLLSVLEAAKMIKPQTLASEKK

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FIGURE 269

ACGGACCGAGGGTTCGAGGGAGGGACACGGACCAGGAACCTGAGCTAGGTCAAAGACGCCCCG
GGCCAGGTGCCCCGTGCGAGGTGCCCCCTGGCCGGAGATGCGGTAGGAGGGGCGAGCGCGAGA
AGCCCCCTTCCTCGGCGCTGCCAACCCGCCACCCAGCCC**ATG**GCGAACCCCGGGCTGGGGCTG
CTTCTGGCGCTGGGCCTGCCGTTCTTGCTGGCCCGCTGGGGCCGAGCCTGGGGGCAAATACA
GACCACTTCTGCAAATGAGAATAGCACTGTTTTGCCTTCATCCACCAGCTCCAGCTCCGATG
GCAACCTGCGTCCGGAAGCCATCACTGCTATCATCGTGGTCTTCTCCCTCTTGGCTGCCTTG
CTCCTGGCTGTGGGGCTGGCACTGTTGGTGCGGAAGCTTCGGGAGAAGCGGCAGACGGAGGG
CACCTACCGGCCCAGTAGCGAGGAGCAGTTCTCCCATGCAGCCGAGGCCCGGGCCCCCTCAGG
ACTCCAAGGAGACGGTGCAGGGCTGCCTGCCCATC**TAG**GTCCCCCTCTCCTGCATCTGTCTCC
CTTCATTGCTGTGTGACCTTGGGGAAAGGCAGTGCCCTCTCTGGGCAGTCAGATCCACCCAG
TGCTTAATAGCAGGGAAGAAGGTACTTCAAAGACTCTGCCCCCTGAGGTCAAGAGAGGATGGG
GCTATTCACCTTTTATATATTTATATAAAATTAGTAGTGAGATGTAAAAAAAAAAAAAAAAAAAA

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FIGURE 270

MANPGLGLLLALGLPFLLARWGRAWGQIQTTSANENSTVLPSSSTSSSSDGNLRPEAITAIIV
VFSLLAALLLAVGLALLVRKLREKRQTEGTYRPSSEEQFSHAAEARAPQDSKETVQGCLPI

099434604
"EST650"

AATATATCATCTATTTATCATTAATCAATAATGTATTCTTTTATTCCAATAACATTTGGGGTT
TTGGGATTTTAAATTTTCAAACACAGCAGAATGACATTTTTTCTGTCACTATTATTATTGTTG
GTATGTGAAGCTATTTGGAGATCCAATTCAGGAAGCAACACATTGGAGAATGGCTACTTTCT
ATCAAGAAATAAAGAGAACCACAGTCAACCCACACAATCATCTTTAGAAGACAGTGTGACTC
CTACCAAAGCTGTCAAAACCACAGGCAAGGGCATAGTTAAAGGACGGAATCTTGACTCAAGA
GGGTTAATTCTTGGTGCTGAAGCCTGGGGCAGGGGTGTAAAGAAAAACACTTAGATTCAATG
ATTGTAAATTTAAGGCAAATACACATATTAGTATTACCTTAGTGTAATGTATCCCTGTCATA
TATACAATAAGGTGAAATTATAAGTACCCTATGCAGTTGGCTGGACAGTCTAAATTGGACT
TTATTAATTTTTTAAAATCAGTAACTGATTTATCACTGGCTATGTGCTTAGATCTACAGGAGA
TCATATAATTTGATACAAATAAAAGAAAAGTGTTCTCTCCCCTTACAGAATTGACATTTTAA
ATGCGATACAGTTAGAATAGGAAATATGACATTAGAAAGGAAGAATGACAGGGAGAAAGGAA
AGAAGGGAAAATGTTGCCAAGGAAAAAAAAA

[illegible]

MTFFLSLLLLLVCEAIWRSNSGSNTLENGYFLSRNKENHSQPTQSSLEDSVTPTKAVKTTGK
GIVKGRNLDSRGLILGAEAWGRGVKKNT

FIGURE 273

GCCAGGAATAACTAGAGAGGAACA**ATG**GGGGTTATTCAGAGGTTTTGTTTTCTCTTAGTTCT
 GTGCCTGCTGCACCAAGTCAAATACTTCCTTCATTAAGCTGAATAATAATGGCTTTGAAGATA
 TTGTCAATTGTTATAGATCCTAGTGTGCCAGAAGATGAAAAATAATGAACAAATAGAGGAT
 ATGGTGACTACAGCTTCTACGTACCTGTTTGAAGCCACAGAAAAAGATTTTTTTTCAAAAA
 TGTATCTATATTAATTCCTGAGAATTGGAAGGAAAATCCTCAGTACAAAAGGCCAAAACATG
 AAAACCATAAACATGCTGATGTTATAGTTGCACCACCTACACTCCCAGGTAGAGATGAACCA
 TACACCAAGCAGTTCACAGAATGTGGAGAGAAAGGCGAATACATTCACTTCACCCCTGACCT
 TCTACTTGGAAAAAACAAAATGAATATGGACCACCAGGCAAACTGTTTGTCCATGAGTGGG
 CTCACCTCCGGTGGGGAGTGTTTGATGAGTACAATGAAGATCAGCCTTTCTACCGTGCTAAG
 TCAAAAAAATCGAAGCAACAAGGTGTTCCGCAGGTATCTCTGGTAGAAATAGAGTTTATAA
 GTGTCAAGGAGGCAGCTGTCTTAGTAGAGCATGCAGAATTGATTCTACAACAAAACGTATG
 GAAAAGATTGTCAATTCCTTCCTGATAAAGTACAACAGAAAAAGCATCCATAATGTTTATG
 CAAAGTATTGATTCTGTTGTTGAATTTTGAACGAAAAAACCCATAATCAAGAAGCTCCAAG
 CCTACAAAACATAAAGTGCAATTTTAGAAGTACATGGGAGGTGATTAGCAATTTCTGAGGATT
 TTA AAAACACCATACCCATGGTGACACCACCTCCTCCACCTGTCTTCTCATTGCTGAAGATC
 AGTCAAAGAATTGTGTGCTTAGTTCTTGATAAGTCTGGAAGCATGGGGGGTAAGGACCGCCT
 AAATCGAATGAATCAAGCAGCAAAACATTTCTGCTGCAGACTGTTGAAAAATGGATCCTGGG
 TGGGGATGGTTCACCTTTGATAGTACTGCCACTATTGTAAATAAGCTAATCCAAATAAAAAAGC
 AGTGATGAAAGAAACACACTCATGGCAGGATTACCTACATATCCTCTGGGAGGAACTCCAT
 CTGCTCTGGAATTAAATATGCATTTTCAAGGTGATTGGAGAGCTACATTCCTCAACTCGATGGAT
 CCGAAGTACTGCTGCTGACTGATGGGGAGGATAACACTGCAAGTTCTTGTATTGATGAAGTG
 AAACAAAGTGGGGCCATTGTTCAATTTTATTGCTTTGGGAAGAGCTGCTGATGAAGCAGTAAT
 AGAGATGAGCAAGATAACAGGAGGAAGTCATTTTATGTTTCAGATGAAGCTCAGAACAATG
 GCCTCATTGATGCTTTTGGGGCTCTTACATCAGGAAATACTGATCTCTCCAGAACTCCCTT
 CAGCTCGAAAGTAAGGGATTAACTGAATAGTAATGCCTGGATGAACGACACTGTCATAAT
 TGATAGTACAGTGGGAAAGGACACGTTCTTTCTCATCACATGGAACAGTCTGCCTCCCAGTA
 TTTCTCTCTGGGATCCCAGTGGAAACAATAATGGAAAATTTACAGTGGATGCAACTTCCAAA
 ATGGCCTATCTCAGTATTCCAGGAACTGCAAAAGGTGGGCACTTGGGCATACAATCTTCAAGC
 CAAAGCGAACCCAGAAACATTAATACTATTACAGTAACCTTCTCGAGCAGCAAAATCTTCTGTGC
 CTCCAATCACAGTGAATGCTAAAATGAATAAGGACGTAAACAGTTTCCCCAGCCCAATGATT
 GTTTACGCAGAAATCTACAAGGATATGTACCTGTTCTTGGAGCCAATGTGACTGCTTTCAT
 TGAATCACAGAATGGACATACAGAAGTTTTGGAACTTTTGGATAATGGTGCAGGCGCTGATT
 CTTTCAAGAATGATGGAGTCTACTCCAGGTATTTTACAGCATATACAGAAATGGCAGATAT
 AGCTTAAAAGTTTCGGGCTCATGGAGGAGCAAACTGCCAGGCTAAAATTACGGCCTCCACT
 GAATAGAGCCGCGTACATACCAGGCTGGGTAGTGAACGGGGAAATTAAGCAAACCCGCCAA
 GACCTGAAATTGATGAGGATACTCAGACCACCTTGGAGGATTTTACGCCGAACAGCATCCGGA
 GGTGCATTTGTGGTATCACAAAGTCCCAAGCCTTCCCTTGCTGACCAATACCCACCAAGTCA
 AATCACAGACCTTGATGCCACAGTTCATGAGGATAAGATTATTCTTACATGGACAGCACCAG
 GAGATAATTTTGTGTTGGAAAAGTTCAACGTTATATCATAAGAATAAGTGCAAGTATTCTT
 GATCTAAGAGACAGTTTTTGTGATGCTCTTCAAGTAAATACTACTGATCTGTCACCAAAGGA
 GGCCAACTCCAAGGAAAGCTTTGCATTTAAACCAGAAAAATATCTCAGAAGAAAATGCAACCC
 ACATATTTATTGCCATTTAAAAGTATAGATAAAAGCAATTTGACATCAAAGTATCCAACATT
 GCACAAGTAACCTTTGTTTATCCCTCAAGCAAACTCTGATGACATTGATCCTACACCTACTCC
 TACTCCTACTCCTACTCCTGATAAAAGTCATAATTCTGGAGTTAATATTTCTACGCTGGTAT
 TGTCTGTGATTGGGTCTGTTGTAATTGTTAACTTTATTTTAAAGTACCACCATT**TGA**ACCTTA
 ACGAAGAAAAAATCTTCAAGTAGACCTAGAAGAGAGTTTTAAAAAACAAAACAATGTAAGT
 AAAGGATATTTCTGAATCTTAAAATTCATCCCATGTGTGATCATAACTCATAAAAAATAATT
 TTAAGATGTCGGAAAAGGATACTTTGATTAAATAAAAAACACTCATGGATATGTAAAAACTGT
 CAAGATTAAAATTTAATAGTTTTATTTATTTGTTATTTTATTTGTAAGAAATAGTGATGAAC
 AAAGATCCTTTTTCTACTGATACCTGGTTGTATATTATTTGATGCAACAGTTTTCTGAAAT
 GATATTTCAAATTCATCAAGAAATTAATCATCTATCTGAGTAGTCAAATAACAAGTAAA
 GGAGAGCAAAATAAACACATTTGGAAAAA AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
 AA

FIGURE 274

MGLFRGFVFLLVLCLLHQSNTSFIKLNNGFEDIVIVIDPSVPEDEKIIIEQIEDMVTASTY
LFEATEKRFFFKNVSILIPENWKENPQYKRPKHENHKHADVIVAPPTLPGRDEPYTKQFTEC
GEKGEYIHFTPDLLLGGKKQNEYGPPGKLFVHEWAHLRWGVFDEYNEDQPFYRAKSKKIEATR
CSAGISGRNRVYKCQGGSCLSRACRIDSTTKLYGKDCQFFPDKVQTEKASIMFMQSIDSVVE
FCNEKTHNQEAPSLQNIKCNFRSTWEVISNSEDFKNTIPMVTPPPPPVFSLKISQRIVCLV
LDKSGSMGGKDRLNRMNQAAKHFLQTVENGSWVGMVHFDSTATIVNKLIQIKSSDERNTLM
AGLPTYPLGGTSICSGIKYAFQVIGELHSQLDGSEVLLLLTDGEDNTASSCIDEVKQSGAIVH
FIALGRAADEAVIEMSKITGGSHFYVSDEAQNNGLIDAFGALTSGNTDLSQKSLQLESKGLT
LNSNAWMNDTVIIDSTVGKDTFFLITWNSLPPSISLWDPSGTIMENFTVDATSKMAYLSIPG
TAKVGTWAYNLQAKANPETLTITVTSRAANSSVPPITVNAKMNDVNSFPSPMIVYAEILQG
YVPVLGANVTAFIESQNGHTEVLELLDNGAGADSFKNMGVYSRYFTAYTENGRYSLKVRAG
GANTARLKLRPPLNRAAYIPGWVNGEIEANPPRPEIDEDTQTTLEDFSRTASGGAFVVSQV
PSLPLPDQYPPSQITDLDATVHEDKIIILTWTAPGDNFDVGKVQRYIIRISASILDLRDSFDD
ALQVNTTDLSPKEANSKESFAFKPENISEENATHIFIAIKSIDKSNLTSKVSNIAQVTLFIP
QANPDDIDPTPTPTPTPTPDKSHNSGVNISTLVLSVIGSVVIVNFILSTTI

Signal peptide:

amino acids 1-21

Putative transmembrane domains:

amino acids 284-300, 617-633

Leucine zipper pattern.

amino acids 469-491, 476-498

N-glycosylation site.amino acids 20-24, 75-79, 340-344, 504-508, 542-546, 588-592,
628-632, 811-815, 832-836, 837-841, 852-856, 896-900

FIGURE 275

CTCCTTAGGTGGAAACCCTGGGAGTAGAGTACTGACAGCAAAGACCGGGAAAGACCATACGTCCCCG
GGCAGGGGTGACAACAGGTGTCTATCTTTTGTATCTCGTGTGTGGCTGCCTTCTTATTTCAAGGAAAG
ACGCCAAGGTAATTTTGACCCAGAGGAGCAATGATGTAGCCACCTCCTAACCTTCCCTTCTTGAACC
CCCAGTTATGCCAGGATTTACTAGAGAGTGTCAACTCAACCAGCAAGCGGCTCCTTCGGCTTAACCTT
GTGGTTGGAGGAGAGAACCCTTTGTGGGGCTGCGTTCTCTTAGCAGTGCTCAGAAGTGACTTGCCTGA
AATGAAGGTGAAAACCTTGGAGATTTCACTTTCAGTCATTGGCTTCTGCCTGCAAGATCATCCTTTAAAA
GTAGAGAAGCTGCTCTGTGTGGTGGTTAACTCCAAGAGGCAGAACTCGTTCTAGAAGGAAATGGATG
CAAGCAGCTCCGGGGGGCCCCAAACGCATGCTTCTGTGGTCTAGCCCAGGGAAGCCCTTCCGTGGGG
GCCCCGGCTTTGAGGGATGCCACCGGTTCTGGACGCATGGCTGATTCTGAATGATGATGTTCCGCC
GGGGGCTGCTTGGCTGGATTTCCCGGGTGGTGGTTTTGCTGGTGGCTCCTCTGCTGTGCTATCTCTGT
CCTGTACATGTTGGCCTGCACCCCAAAAGGTGACGAGGAGCAGCTGGCACTGCCAGGGGCCAACAGC
CCCACGGGGAAGGAGGGGTACCAGGCCGCTCCTTCAGGAGTGGGAGGAGCAGCACCGCAACTACGTGA
GCAGCCTGAAGCGGCAGATCGCACAGCTCAAGGAGGAGCTGCAGGAGAGGAGTGAGCAGCTCAGGAA
TGGGCGATACCAAGCCAGCGATGCTGGCCTGGGTCTGGACAGGAGCCCCCAGAGAAAACCCAG
GCCGACCTCCTGGCCTTCTGCACTCGCAGGTGGACAAGGCAGAGGTGAATGCTGGCGTCAAGCTGG
CCACAGAGTATGCAGCAGTGCTTTTCGATAGCTTTACTCTACAGAAGGTGTACCAGCTGGAGACTGG
CCTTACCCGCCACCCCGAGGAGAAGCCTGTGAGGAAGGACAAGCGGGATGAGTTGGTGAAGCCATT
GAATCAGCCTTGGAGACCCTGAACAATCCTGCAGAGAACAGCCCCAATCACCGTCTTACACGGCCT
CTGATTTTCATAGAAGGGATCTACCGAACAGAAAGGGACAAAGGGACATTGTATGAGCTCACCTTCAA
AGGGGACCACAAACACGAATTCAAACGGCTCATCTTATTTTCGACCATTACGCCCCATCATGAAAGTG
AAAAATGAAAAGCTCAACATGGCCCAACACGCTTATCAATGTTATCGTGCCTCTAGCAAAAAGGGTGG
ACAAGTTCCGGCAGTTCATGCAGAATTTCAAGGAGATGTGCATTGAGCAGGATGGGAGAGTCCATCT
CACTGTTGTTTACTTTGGGAAAGAAGAAATAAATGAAGTCAAAGGAATACTTGAAAACACTTCCAAA
GCTGCCAACTTCAGGAACCTTACCTTCATCCAGCTGAATGGAGAATTTCTCGGGAAAGGGACTTG
ATGTTGGAGCCCGCTTCTGGAAAGGGAAGCAACGCTCCTTCTCTTTTTCTGTGATGTGGACATCTACTT
CACATCTGAATTCCTCAATACGTGTAGGCTGAATACACAGCCAGGGAAGAAGGTATTTTATCCAGTT
CTTTTCAGTCAGTACAATCCTGGCATAATATACGGCCACCATTGATGCAGTCCCTCCCTTGGAAACAGC
AGCTGGTCATAAAGAAGGAAACTGGATTTTGGAGAGACTTTGGATTTGGGATGACGTGTAGTATCG
GTCAGACTTCATCAATATAGGTGGGTTTGTATCTGGACATCAAAGGCTGGGGCGGAGAGGATGTGCAC
CTTTATCGCAAGTATCTCCACAGCAACCTCATAGTGGTACGGACGCCTGTGCGAGGACTCTTCCACC
TCTGGCATGAGAAGCGCTGCATGGACGAGCTGACCCCCGAGCAGTACAAGATGTGCATGCAGTCCAA
GGCCATGAACGAGGCATCCACGGCCAGCTGGGCATGCTGGTGTTCAGGCACGAGATAGAGGCTCAC
CTTCGCAAAACAGAAACAGAAAGACAAGTAGCAAAAAACATGAACCTCCAGAGAAGGATTGTGGGAGA
CACTTTTTTCTTTCTTTTGAATTAAGTGGCTGCAACAGAGAAAAGACTTCCATAAAGGACG
ACAAAAGAATTGGACTGATGGGTGAGAGATGAGAAAGCCTCCGATTTCTCTCTGTTGGGCTTTTTAC
AACAGAAATCAAAATCTCCGCTTGGCTGCAAAAGTAACCCAGTTGCAACCCTTGCAAGTGTCTGACA
AAGGCAGAATGCTTGTGAGATTATAAGCCTAATGGTGTGGAGGTTTTGATGGTGTTTACAATACACT
GAGACCTGTTGTTTTGTGTGCTCATTGAAATATTTCATGATTTAAGAGCAGTTTTGTAAAAAATTCAT
TAGCATGAAAGGCAAGCATATTTCTCCTCATATGAATGAGCCTATCAGCAGGGCTCTAGTTTCTAGG
AATGCTAAAAATATCAGAAGGCAGGAGAGGAGATAGGCTTATTATGATACTAGTGAGTACATTAAGTA
AAATAAAATGGACCAGAAAAGAAAAGAAACCATAAATATCGTGTCTATTTTTCCCAAGATTAAACCA
AAAATAATCTGCTTATCTTTTTGGTTGTCTTTTAACTGTCTCCGTTTTTTCTTTTATTTAAAAAT
GCACTTTTTTTTCCCTTGTGAGTTATAGTCTGCTTATTTAATTACCACTTTGCAAGCCTTACAAGAGA
GCACAAGTTGGCCTACATTTTTTATATTTTTTAAGAAGATACTTTGAGATGCATTATGAGAACTTTCA
GTTCAAAGCATCAAATTGATGCCATATCCAAGGACATGCCAAATGCTGATTCTGTGAGGCACTGAAT
GTCAGGCATTGAGACATAGGGAAGGAATGGTTTGTACTAATAACAGACGTACAGATACTTTCTCTGAA
GAGTATTTTTCGAAGAGGAGCAACTGAACACTGGAGGAAAAGAAAATGACACTTTCTGCTTTACAGAA
AAGGAAACTCATTACAGCTGGTGATATCGTGATGTACCTAAAAGTCAGAAACCACATTTTCTCCTCA
GAAGTAGGGACCGCTTCTTACCTGTTTAAATAAACCAGGATATACCGTGTGAACCAACAATCTCT
TTTCAAAACAGGGTGTCTCTCTGGCTTCTGGCTTCCATAAGAAGAAATGGAGAAAATATATATAT
ATATATATATATTGTGAAAGATCAATCCATCTGCCAGAAATCTAGTGGGATGGAAGTTTTTGTCTACAT
GTTATCCACCCCAGGCCAGGTGGAAGTAACTGAATATTTTTTAAATTAAGCAGTTCTACTCAATCA
CCAAGATGCTTCTGAAAATTGCATTTTATTACCATTTCAAACATTTTTTAAAAATAAATACAGTTA
ACATAGAGTGGTTCTTCTTCTTCTGATGTGAAAATATTAGCCAGCACCAGATGCATGAGCTAATTTCT
CTTTGAGTCTTGTCTTCTGTTTGTGCTCACAGTAACTCATTTGTTTAAAGCTTCAAGAACATTCAAGC
TGTTGGTGTGTTAAAAATGCATTGTATTGATTTGTACTGGTAGTTTATGAAATTTAATTAAAACAC
AGGCCATGAATGGAAGGTGGTATTGCACAGCTAATAAAATATGATTTGTGGATATGAA

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FIGURE 276

MMMVRRGLLAWISRVVLLVLLCCAISVLYMLACTPKGDEEQ LALPRANSPTGKEGYQAVLQ
EWEEQHRNYVSSLKRQIAQLKEELQERSEQLRNGQYQASDAAGLGLDRSPPEKTQADLLAFL
HSQVDKAEVNAGVKLATEYA AVPFDSFTLQKVYQLETGLTRHP EKPVRKDKRDELVEAIES
ALET LNNPAENSPNHRPYTASDFIEGIYRTERDKGTLYELTFKGDHKHEFKRLILFRPFSP I
MKVKNEKLN MANTLINVIVPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVYFGKEEINEVK
GILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLN TCR
LNTQPGKKVFYPVLFSQYNPGIIYGHHD AVPPLEQQLV IKKETGFWRDFGFGMTCQYRSDFI
NIGGFDDL DIKGWGGEDVHLYRKYLHSNLIVVRTPVRGLFHLWHEKRCMDELTPEQYKMCMQS
KAMNEASHGQLGMLVFRHEIEAHLRKQKQKTSSKKT

FIGURE 276

GAAAGA**ATG**TTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACC
AGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCAT
ATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA
GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCTACTTTGCAATGTAACCCAGAGGGT
ATCATTCTGGTTTGTGGTTACAGACCCCTTCAAAAAATCACACCCCTTCCTGCTGTTGAGGTGC
AATCAGCCATAAGAATGAACAAGAACC GGATCAACAATGCCTTCTTTCTAAATGACCAAAC
CTGGAATTTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTGCCCATCTG
GATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTACTGATTTTAT
CAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAATGACGCTGAAGAT
AAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCCTCTGATCCCCCTGGACATGAAGGG
GGGCATATTAATGATGCCTTCA**TGA**CAGAGGATGAGAGGGCTCACCCCTCTCTGAAGGGCTGT
TGTTCTGCTTCCTCAAGAAATTAAACATTTGTTTCTGTGTGACTGCTGAGCATCCTGAAATA
CCAAGAGCAGATCATATATTTTGTTCACCATTCTTCTTTTGTAATAAATTTTGAATGTGCT
TGAAAGTGAAAAGCAATCAATTATACCCACCAACACCACTGAAATCATAAGCTATTCACGAC
TCAAAATATTCTAAAATATTTTTTCTGACAGTATAGTGTATAAATGTGGTCATGTGGTATTTG
TAGTTATTGATTTAAGCATTTTTTAGAAATAAGATCAGGCATATGTATATATTTTCACTTC
AAAGACCTAAGGAAAAATAAATTTTCCAGTGGAGAATACATATAATATGGTGTAGAAATCAT
TGAAAATGGATCCTTTTTTGACGATCACTTATATCACTCTGTATATGACTAAGTAAACAAAAG
TGAGAAGTAATTATTGTAAATGGATGGATAAAAAATGGAATTACTCATATACAGGGTGGAAATT
TTATCCTGTTATCACACCAACAGTTGATTATATATTTTTCTGAATATCAGCCCCTAATAGGAC
AATTCTATTTGTTGACCATTTCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAG
TAATAATCATCTCTTTTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 278

MLWLLFFLVTAIHAELCQPGAENAFKVRLSIRTALGDKAYAWDTNEEYLFKAMVAFSMRKVP
NREATEISHVLLCNVTQRVSEFWFVVDPSKNHTLPAVEVQSAIRMNKNRINNAFFLNDQTL
FLKIPSTLAPPMDPSVPIWIIIFGVIFCIIIVAIALLLSGIWQRRRKNKEPSEVDDAEDKC
ENMITIENGIPSDPLDMKGGILMMPS

09944-14604
T0944-14604

AACTCAAACCTCCTCTCTCTGGGAAAACGCGGTGCTTGCTCCTCCCGGAGTGGCCTTGGCAGG
GTGTTGGAGCCCTCGGTCTGCCCCGTCCGGTCTCTGGGGCCAAGGCTGGGTTTCCCTC**ATGT**
ATGGCAAGAGCTCTACTCGTGCGGTGCTTCTTCTCCTTGGCATAACAGCTCACAGCTCTTTGG
CCTATAGCAGCTGTGGAAATTTATACCTCCCGGGTGCTGGAGGCTGTTAATGGGACAGATGC
TCGGTTAAATGCACTTTCTCCAGCTTTGCCCCCTGTGGGTGATGCTCTAACAGTGACCTGGA
ATTTTCGTCCTCTAGACGGGGGACCTGAGCAGTTTGTATTCTACTACCACATAGATCCCTTC
CAACCCATGAGTGGGCGGTTTAAGGACCGGGTGTCTTGGGATGGGAATCCTGAGCGGTACGA
TGCCTCCATCCTTCTCTGGAAACTGCAGTTCGACGACAATGGGACATACACCTGCCAGGTGA
AGAACCCACCTGATGTTGATGGGGTGATAGGGGAGATCCGGCTCAGCGTCGTGCACACTGTA
CGCTTCTCTGAGATCCACTTCCTGGCTCTGGCCATTGGCTCTGCCTGTGCACTGATGATCAT
AATAGTAATTGTAGTGGTCCTCTTCCAGCATTACCGGAAAAAGCGATGGGCCGAAAGAGCTC
ATAAAGTGGTGGAGATAAAATCAAAGAAGAGGAAAGGCTCAACCAAGAGAAAAAGGTCTCT
GTTTATTTAGAAGACACAGAC**TAA**CAATTTTAGATGGAAGCTGAGATGATTTCCAAGAACAA
GAACCCTAGTATTTCTTGAAGTTAATGGAACTTTTCTTTGGCTTTTCCAGTTGTGACCCGT
TTTCCAACCAGTTCTGCAGCATATTAGATTCTAGACAAGCAACACCCCTCTGGAGCCAGCAC
AGTGCTCCTCCATATCACCAGTCATACACAGCCTCATTATTAAGGTCTTATTTAATTTCAGA
GTGTAAATTTTTTCAAGTGCTCATTAGGTTTTATAAACAAGAAGCTACATTTTTTGCCCTTAA
GACACTACTTACAGTGTTATGACTTGTATACACATATATTGGTATCAAAGGGGATAAAAGCC
AATTTGTCTGTTACATTTCCTTTCACGTATTTCTTTTAGCAGCACTTCTGCTACTAAAGTTA
ATGTGTTTACTCTCTTCCCTTCCCACATTCTCAATTAAAAGGTGAGCTAAGCCTCCTCGGTG
TTTCTGATTAACAGTAAATCCTAAATTCAACTGTAAATGACATTTTTTATTTTTATGTCTC
TCCTTAACTATGAGACACATCTTGTTTTACTGAATTTCTTTCAATATTCAGGTGATAGATT
TTTGTGCG

FIGURE 280

MYGKSSTRAVLLLLGIQLTALWPAAVEIYTSRVLEAVNGTDARLKCTFSSFAPVGDALTVT
WNFRPLDGGPEQFVFYYHIDPFQPMGRFKDRVSWDGNPERYDASILLWKLQFDDNGTYTCQ
VKNPPDVGVIQEIRLSVVHTVRFSEIHFLALAIGSACALMIIIVIVVVLQHYRKKRWAER
AHKVVEIKSKEERLNQEKKVSVYLEDTD

FIGURE 280

FIGURE 281

GCATTTTTGTCTGTGCTCCCTGATCTTCAGGTCACCACCATGAAGTTCTTAGCAGTCCTGGT
ACTCTTGGGAGTTTCCATCTTTCTGGTCTCTGCCCAGAATCCGACAACAGCTGCTCCAGCTG
ACACGTATCCAGCTACTGGTCCTGCTGATGATGAAGCCCCTGATGCTGAAACCACTGCTGCT
GCAACCACTGCGACCACTGCTGCTCCTACCACTGCAACCACCGCTGCTTCTACCACTGCTCG
TAAAGACATTCCAGTTTTACCCAAATGGGTTGGGGATCTCCCGAATGGTAGAGTGTGTCCCTT
GAGATGGAATCAGCTTGAGTCTTCTGCAATTGGTCACAACCTATTCATGCTTCCTGTGATTTC
ATCCAACCTACTTACCTTGCCCTACGATATCCCCCTTTATCTCTAATCAGTTTATTTTCTTTCAA
ATAAAAAATAACTATGAGCAACATAAAAAAAAAAAAAA

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FIGURE 282

MKFLAVLVLLGVSI FLVSAQNPTTAAPADTYPATGPADDEAPDAETTAAATTATTAAPTAT
TAASTTARKDIPVLPKWVGDL PNGRVCP

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60

FIGURE 283

GGACTCTGAAGGTCCCAAGCAGCTGCTGAGGCCCCCAAGGAAGTGGTTCCAACCTTGGACCC
CTAGGGGTCTGGATTTGCTGGTTAACAAGATAACCTGAGGGCAGGACCCCATAGGGGA**ATGC**
TACCTCCTGCCCTTCCACCTGCCCTGGTGTTCACGGTGGCCTGGTCCCTCCTTGCCGAGAGA
GTGTCCTGGGTGAGGGACGCAGAGGACGCTCACAGACTCCAGCCCTTTGTTACCGAGAGGAC
ACTTGGAAGGTCCAGCGATGGTCCGGAGTCCACACACAGACTGGCGGCAGGGCAGGAGGGG
GACAGTTCTGTTGTGCTTGGTTGGACAGTAAGAGGGTCTTGGCCAGTCCAGGGTGGGGGGCG
GCAAACCTCATAAAGAACCAGAGGGTCTGGGCCCCGCCACAGAGTCATCTGCCAGCTCCT
CTGCTGCTGGCCAGTGGGAGTGGCACGAGGTGGGGCTTTGTGCCAG**TAAA**ACCACAGGCTGG
ATTTGCCTGCGGGCCATGGTCCCTGTCTAGGGCAGCAATTCTCAACCTTCTTGCTCTCAGGA
CCCCAAAGAGCTTTCATTGTATCTATTGATTTTTACCACATTAGCAATTAAACTGAGAAAT
GGGCCGGGCACGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGGTGGAT
CACCTGAGATCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAAACCTTGTCTACTAAAAA
TACAAAAAATTAGCCAGGCACAGTGGTGTGCACTGGTAGTCCCAGTTACTCGGGAGGCTGAG
GCAGGAAAATCGCTTGAACCCAGGAGGCGGACGTTGCGGTGAGCCGAGATCGCGCCGCTGAT
TCCAGCCTGGGCGACAAGAGTGAGACTCCATCTCACACA

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FIGURE 284

MLPPALPPALVFTVAWSLLAERVSWVRDAEDAHRLQPFVTERTLGKVQRWSGVHTQTGGRAG
GGQFCCAWLDSKRVLASPGWGAANSIKNQRVWAPATESSAQLLCCWPVGVARGGALCQ

FIGURE 284

FIGURE 285

GTC**ATG**CCAGTGCCTGCTCTGTGCCTGCTCTGGGCCCTGGCAATGGTGACCCGGCCTGCCTCA
GCGGCCCCCATGGGCGGCCAGAACTGGCACAGCATGAGGAGCTGACCCTGCTCTTCCATGG
GACCCTGCAGCTGGGCCAGGCCCTCAACGGTGTGTACAGGACCACGGAGGGACGGCTGACAA
AGGCCAGGAACAGCCTGGGTCTCTATGGCCGCACAATAGAACTCCTGGGGCAGGAGGTCAGC
CGGGGCCGGGATGCAGCCCAGGAAC TTCGGGCAAGCCTGTTGGAGACTCAGATGGAGGAGGA
TATTCTGCAGCTGCAGGCAGAGGCCACAGCTGAGGTGCTGGGGGAGGTGGCCCAGGCACAGA
AGGTGCTACGGGACAGCGTGCAGCGGCTAGAAGTCCAGCTGAGGAGCGCCTGGCTGGGCCCT
GCCTACCGAGAATTTGAGGTCTTAAAGGCTCACGCTGACAAGCAGAGCCACATCCTATGGGC
CCTCACAGGCCACGTGCAGCGGCAGAGGCGGGAGATGGTGGCACAGCAGCATCGGCTGCGAC
AGATCCAGGAGAGACTCCACACAGCGGCGCTCCCAGCC**TGA**ATCTGCCTGGATGGA ACTGAG
GACCAATCATGCTGCAAGGAACACTTCCACGCCCCGTGAGGCCCTGTGCAGGGAGGAGCTG
CCTGTTCACTGGGATCAGCCAGGGCGCCGGGCCCCACTTCTGAGCACAGAGCAGAGACAGAC
GCAGGCGGGGACAAAGGCAGAGGATGTAGCCCCATTGGGGAGGGGTGGAGGAAGGACATGTA
CCCTTTCATGCCTACACACCCCTCATTAAAGCAGAGTCGTGGCATTTCAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 286

MPVPALCLLWALAMVTRPASAAPMGGPELAQHEELTLLFHGTLQLGQALNGVYRTTEGRLTK
ARNSLGLYGRRTIELLGQEVSRGRDAAQELRASLLETQMEEDILQLQAEATAEVLGEVAQAQK
VLRDSVQRLEVQLRSAWLGPAYREFEVLKAHADKQSHILWALTGHVQRQRREMVAAQQHRLRQ
IQERLHTAALPA

GGCAAC**ATG**GCTCAGCAGGCTTGCCCCAGAGCCATGGCAAAGAATGGACTTGTAATTTGCAT
CCTGGTGATCACCTTACTCCTGGACCAGACCAGCCACACATCCAGATTAAAAGCCAGGA
AGCACAGCAAACGTCGAGTGAGAGACAAGGATGGAGATCTGAAGACTCAAATTGAAAAGCTC
TGGACAGAAGTCAATGCCTTGAAGGAAATTC AAGCCCTGCAGACAGTCTGTCTCCGAGGCAC
TAAAGTTCACAAGAAATGCTACCTTGCTTCAGAAGGTTTGAAGCATTTCCATGAGGCCAATG
AAGACTGCATTTCCAAAGGAGGAATCCTGGTTATCCCCAGGAACCTCGACGAAATCAACGCC
CTCCAAGACTATGGTAAAAGGAGCCTGCCAGGTGTCAATGACTTTTGGCTGGGCATCAATGA
CATGGTCACGGAAGGCAAGTTTGTGTGACGTCAACGGAATCGCTATCTCCTTCCTCAACTGGG
ACCGTGACAGCCTAACGGTGGCAAGCGAGAAAACCTGTGTCTCTGTTCTCCAATCAGCTCAG
GGCAAGTGGAGTGATGAGGCCTGTGCGAGCAGCAAGAGATACATATGCGAGTTCACCATCCC
TAA**ATAG**GTCTTTCTCCAATGTGTCTCTCCAAGCAAGATTCATCATAACTTATAGGTTTCATGA
TCTCTAAGATCAAGTAAAAATCATAATTTTTTACTTATTAAAAAATTGCAACACAAGATCAAT
GTCCATAGCAATATGATAGCATCAGCCAATTTTGCTAACACATTTCTTTGGGATTTTGCCCT
TCCTGGGGTATAGGGGATCAGAAATATTGATCCATGTGCACGCAGATAAAATGGCTTCTGCT
AAACAGACTAAAATCTTTCTCTCTAGTCTTTCTCACTTGTAACAAACCCAGTTTGTTTTCAA
AAATCACAGTAGCAATGCAACTCATCACTCTAGAAAAGCAAGCTTAGGCTACCTGAAAGATT
TTCCCTTGGAAGTTTAGCGTATGTTTGACTAACAAAAATTCCTTACATCAGAGACTCTAGGT
GCTATATAATCCAAAAACTTTTCAGCCTGTTGCTCATTCTGTCCCATGCTGGCAATAATACC
TTGTCAGCCCATTACCCTTATTTTGAATTGCTCCATCTCCTGGTGGGACTTGATCTTGTCT
GCCATATCAGAACACAAACCCCTGAAGAGGTTCTGATTTGATTTTTTTTTTTTCTTCATGCC
TACCCTTTTTTTTGAAGTTTCCAGCCGCAATTTGAAATGAAATGACAAGGTGTATATTTGAT
CAATTTTCATTCCCACCATTGCATTACAACCTCTAACTTAAATGGGTAACCCTAAGGCATAT
CAAAGAAGCAGATTGCATGATAAACGGAATAGAAAAAAGAACCTACATTTATTTTGCTTT
AGCATCCTTACTCTCACCTTTTATGAGATTGAGAGTGGACTTACATTTCTTTTTTACATTT
TCGTATATTTATTTTTTTTAGCCATCATTATATGTTTAAGTCTATTATGGGCAACCAATCTT
TGGAAGCTGAAAACCTGAATTTAAAGAATGCTATCTTGGAAAATTGCATACGTCTGTGCAATT
TTTTATTCTGCCTAGTGCTATTCTGCTTGTTTAACTAGATTGTACAAAATAACTTCATTGCT
TAATATCAAATTACAAAGTTTAGACTTGGAGGGAAATGGGCTTTTTTAGAAGCAAACAATTTT
AAATATATTTTGTTCTTCAAATAAATAGTGTTTAAACATTGAATGTGTTTTGTGAACAATAT
CCCACTTTGCAAACCTTAACTACACATGCTTGGAATTAAGTTTTAGCTGTTTTTCATTGCTCA
ATAATAAAGCCTGAATTTCTGATCAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

MAQQACPRAMAKNGLVICILVITLLLDQTTSHSRLKARKHSKRRVRDKDGLKTQIEKLWT
EVNALKEIQALQTVCLRGTKVHKKCYLASEGLKHFHEANEDCISKGGILVIPRNSDEINALQ
DYGKRSLPGVNDFWLGINDMVTEGKFVDVNGIAISFLNWDRAQPNGGKRENCVLFSQSAQ GK
WSDEACRSSKRYICEFTIPK

[illegible]

FIGURE 289

GCGAGGACCGGGTATAAGAAGCCTCGTGGCCTTGCCCGGGCAGCCGCAGGTTCCCCGCGCGC
CCCGAGCCCCCGCGCC**ATGA**AGCTCGCCGCCCTCCTGGGGCTCTGCGTGGCCCTGTCCTGCA
GCTCCGCTGCTGCTTTCTTAGTGGGCTCGGCCAAGCCTGTGGCCCAGCCTGTCGCTGCGCTG
GAGTCGGCGGCGGAGGCCGGGGCCGGGACCCTGGCCAACCCCCTCGGCACCCTCAACCCGCT
GAAGCTCCTGCTGAGCAGCCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCCAGAAGT
GTGTGGCTGAGCTGGGTCCCCAGGCCGTGGGGGCCGTGAAGGCCCTGAAGGCCCTGCTGGGG
GCCCTGACAGTGTGGCT**TGA**GCCGAGACTGGAGCATCTACACCTGAGGACAAGACGCTGCC
CACCCGCGAGGGCTGAAAACCCCGCCGCGGGGAGGACCGTCCATCCCCTTCCCCGGCCCCCT
CTCAATAAACGTGGTTAAGAGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAA

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FIGURE 290

MKLAALLGLCVALSCSSAAFLVGSAPVAQPVAALESAAEAGAGTLANPLGTNLPLKLLS
SLGIPVNHLEGSQKCVAELGPQAVGAVKALKALLGALTIVFG

103111 121660

FIGURE 291

TGAAGGACTTTTCCAGGACCCAAGGCCACACACTGGAAGTCTTGCAGCTGAAGGGAGGCACT
 CCTTGGCCTCCGCAGCCGATCAC**ATGA**AGGTGGTGCCAAGTCTCCTGCTCTCCGTCCTCCTG
 GCACAGGTGTGGCTGGTACCCGGCTTGGCCCCCAGTCCTCAGTCGCCAGAGACCCCAGCCCC
 TCAGAACCAGACCAGCAGGGTAGTGCAGGCTCCAGGGAGGAAGAGGAAGATGAGCAGGAGG
 CCAGCGAGGAGAAGGCCGGTGAGGAAGAGAAAGCCTGGCTGATGGCCAGCAGGCAGCAGCTT
 GCCAAGGAGACTTCAAACCTTCGGATTTCAGCCTGCTGCGAAAGATCTCCATGAGGCACGATGG
 CAACATGGTCTTCTCTCCATTTGGCATGTCTTGGCCATGACAGGCTTGATGCTGGGGGCCA
 CAGGGCCGACTGAAACCCAGATCAAGAGAGGGCTCCACTTGCAGGCCCTGAAGCCCACCAAG
 CCCGGGCTCCTGCCTTCCCTCTTTAAGGGACTCAGAGAGACCCTCTCCCGCAACCTGGAAC
 GGGCCTCTCACAGGGGAGTTTTGCCTTCATCCACAAGGATTTTGATGTCAAAGAGACTTTCT
 TCAATTTATCCAAGAGGTATTTTGATACAGAGTGCCTGCCTATGAATTTTCGCAATGCCTCA
 CAGGCCAAAAGGCTCATGAATCATTACATTAACAAAGAGACTCGGGGGAAAATTCCCAAAC
 GTTTGATGAGATTAATCCTGAAACCAAATTAATTCTTGTGGATTACATCTTGTTCAAAGGGA
 AATGGTTGACCCCATTTGACCCTGTCTTCACCGAAGTCGACACTTTCCACCTGGACAAGTAC
 AAGACCATTAAGGTGCCCATGATGTACGGTGCAGGCAAGTTTGCCTCCACCTTTGACAAGAA
 TTTTCGTTGTCTATGTCTCAAACCTGCCCTACCAAGGAAATGCCACCATGCTGGTGGTCTCA
 TGGAGAAAATGGGTGACCACCTCGCCCTTGAAGACTACCTGACCACAGACTTGGTGGAGACA
 TGGCTCAGAAACATGAAAACAGAAACATGGAAGTTTTCTTTCCGAAGTTCAAGCTAGATCA
 GAAGTATGAGATGCATGAGCTGCTTAGGCAGATGGGAATCAGAAGAATCTTCTCACCTTTG
 CTGACCTTAGTGAACCTCTCAGCTACTGGAAGAAATCTCCAAGTATCCAGGGTTTTACGAAGA
 ACAGTGATTGAAGTTGATGAAAGGGGCACTGAGGCAGTGGCAGGAATCTTGTCAGAAATTAC
 TGCTTATTCCATGCCTCCTGTCTATCAAAGTGGACCGGCCATTTTCATTTTCATGATCTATGAAG
 AAACCTCTGGAATGCTTCTGTTTCTGGGCAGGGTGGTGAATCCGACTCTCCTAT**TAA**TTCAGG
 ACATGCATAAGCACTTCGTGCTGTAGTAGATGCTGAATCTGAGGTATCAAACACACACAGGA
 TACCAGCAATGGATGGCAGGGGAGAGTGTTCTTTTTGTTCTTAACTAGTTTTAGGGTGTCTC
 AAATAAATACAGTAGTCCCCACTTATCTGAGGGGGATACATTCAAAGACCCCCAGCAGATGC
 CTGAAACGGTGGACAGTGCTGAACCTTATATATATTTTTTCTACACATACATACCTATGAT
 AAAGTTTAATTTATAAATTAGGCACAGTAAGAGATTAACAATAATAACAACATTAAGTAAAA
 TGAGTTACTTGAACGCAAGCACTGCAATACCATAACAGTCAAACCTGATTATAGAGAAGGCTA
 CTAAGTGACTCATGGGCGAGGAGCATAGACAGTGTGGAGACATTGGGCAAGGGGAGAATTCA
 CATCCTGGGTGGGACAGAGCAGGACGATGCAAGATTCATCCCACTACTCAGAATGGCATGC
 TGCTTAAGACTTTTAGATTGTTTATTTCTGGAATTTTTTCATTTAATGTTTTTGGACCATGGT
 TGACCATGGTTAACTGAGACTGCAGAAAGCAAACCATGGATAAGGGAGGACTACTACAAAA
 GCATTAAATTGATACATATTTTTTAAAAA

MKVVP
 SLLLSVLLAQVWLV
 PGLAPSPQSPET
 PAPQNQTSRVVQAP
 REEEEEEDEQEASE
 SEEKAGE
 EEKAWLMASRQQL
 AKETSNGFGLLRKI
 SMRHDGNMVFS
 PFGMSLAMTGLML
 GATGPTETQI
 KRGLHLQALKPTK
 PGLLPSLFLKGLR
 ETLSRNLELGLS
 QGSFAFIHKDFD
 VKETFFNLSKRYF
 DTECVPMNFRNAS
 QAKRLMNHYINK
 ETRGKIPKLFDE
 INPETKLILVDY
 ILFKGKWLT
 PFDP
 VFTEVDTFHLDKY
 KTIKVPMMYGAGK
 FASTFDKNFRCH
 VLKLPYQGNATML
 VVLMEKMGDHL
 ALEDYLTTDLVET
 WLRNMKTRNMEV
 FFFPKFKLDQKY
 EMHELLRQMGIR
 RIFSPFADLSELS
 A
 TGRNLQVSRVLR
 RTVIEVDERGTEA
 VAGILSEITAYSM
 PPVIKVDRPFHF
 MIIYEETSGMLLF
 LGRV
 VNPTLL

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FIGURE 294

MRRLLLVTSLVVVLLWEAGAVPAPKVPIKMQVKHWPSEQDPEKAWGARVVEPPEKDDQLVVL
FPVQKPKLLTTEEKPRGQGRGPILPGTKAWMETEDTLGRVLSPEPDHDSLYHPPPEEDQGEE
RPRLWVMPNHQVLLGPEEDQDHIYHPQ

1. 2. 3. 4. 5. 6. 7. 8. 9. 10. 11. 12. 13. 14. 15. 16. 17. 18. 19. 20. 21. 22. 23. 24. 25. 26. 27. 28. 29. 30. 31. 32. 33. 34. 35. 36. 37. 38. 39. 40. 41. 42. 43. 44. 45. 46. 47. 48. 49. 50. 51. 52. 53. 54. 55. 56. 57. 58. 59. 60.

FIGURE 295

AGAAAGCTGCACTCTGTTGAGCTCCAGGGCGCAGTGGAGGGAGGGAGTGAAGGAGCTCTCTG
TACCCAAGGAAAGTGCAGCTGAGACTCAGACAAGATTACAATGAACCAACTCAGCTTCCTGC
TGTTTCTCATAGCGACCACCAGAGGATGGAGTACAGATGAGGCTAATACTTACTTCAAGGAA
TGGACCTGTTCTTCGTCTCCATCTCTGCCCAGAAGCTGCAAGGAAATCAAAGACGAATGTCC
TAGTGCATTTGATGGCCTGTATTTTCTCCGCACTGAGAATGGTGTATCTACCAGACCTTCT
GTGACATGACCTCTGGGGGTGGCGGCTGGACCCTGGTGGCCAGCGTGCATGAGAATGACATG
CGTGGGAAGTGCACGGTGGGCGATCGCTGGTCCAGTCAGCAGGGGCAGCAAAGCAGACTACCC
AGAGGGGGACGGCAACTGGGCCAACTACAACACCTTTGGATCTGCAGAGGCGGCCACGAGCG
ATGACTACAAGAACCCTGGCTACTACGACATCCAGGCCAAGGACCTGGGCATCTGGCACGTG
CCCAATAAGTCCCCCATGCAGCACTGGAGAAACAGCTCCCTGCTGAGGTACCGCACGGACAC
TGGCTTCCTCCAGACACTGGGACATAATCTGTTTGGCATCTACCAGAAATATCCAGTGAAAT
ATGGAGAAGGAAAGTGTTGGACTGACAACGGCCCGGTGATCCCTGTGGTCTATGATTTTGGC
GACGCCCAGAAAACAGCATCTTATTACTCACCTATGGCCAGCGGGAATTCAGTGCGGGATT
TGTTTCAGTTCAGGGTATTTAATAACGAGAGAGCAGCCAACGCCTTGTGTGCTGGAATGAGGG
TCACCGGATGTAACTGAGCATCACTGCATTGGTGGAGGAGGATACTTTCCAGAGGCCAGT
CCCCAGCAGTGTGGAGATTTTCTGGTTTTGATTGGAGTGGATATGGAACCATGTTGGTTA
CAGCAGCAGCCGTGAGATAACTGAGGCAGCTGTGCTTCTATTCTATCGTTGAGAGTTTTGTG
GGAGGGAACCCAGACCTCTCCTCCCAACCATGAGATCCCAAGGATGGAGAACAACCTTACCCA
GTAGCTAGAATGTTAATGGCAGAAGAGAAAACAATAAATCATATTGACTCAAGAAAAAAA

FIGURE 296

MNQLSFLLFLIATTRGWSTDEANTYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRTEN
GVIYQTFCDMTSGGGGWTLVASVHENDMRGKCTVGDRWSSQQGSKADYPEGDGNWANYNTFG
SAEAATSDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSSLLRYRTDTGFLQTLGHNLFGI
YQKYPVKYGEGKCWTDNGPVI PVVYDFGDAQKTASYYSPIYGQREFTAGFVQFRVFNNERAAN
ALCAGMRVTGCNTEHHCIGGGGYFPEASPQQCGDFSGFDWSGYGTHVGYSRSSREITEAAVLL
FYR

T.D.S.T. = T.D.T. 6560

FIGURE 297

GCGGAGCCGGCGCCGGCTGCGCAGAGGAGCCGCTCTCGCCGCCGCCACCTCGGCTGGGAGCC
 CACGAGGCTGCCGCATCCTGCCCTCGGAACA**ATG**GGACTCGGCGCGCGAGGTGCTTGGGCCG
 CGCTGCTCCTGGGGACGCTGCAGGTGCTAGCGCTGCTGGGGGCCGCCCATGAAAGCGCAGCC
 ATGGCGGCATCTGCAAACATAGAGAATTCTGGGCTTCCACACAACCTCCAGTGCTAACTCAAC
 AGAGACTCTCCAACATGTGCCTTCTGACCATACAAATGAAACTTCCAACAGTACTGTGAAAC
 CACCAACTTCAGTTGCCTCAGACTCCAGTAATACAACGGTCACCACCATGAAACCTACAGCG
 GCATCTAATACAACAACACCAGGGATGGTCTCAACAAATATGACTTCTACCACCTTAAAGTC
 TACACCCAAAACAACAAGTGTTTACAGAACACATCTCAGATATCAACATCCACAATGACCG
 TAACCCACAATAGTTTCAGTGACATCTGCTGCTTCATCAGTAACAATCACAACAACCTATGCAT
 TCTGAAGCAAAGAAAGGATCAAAATTTGATACTGGGAGCTTTGTTGGTGGTATTGTATTAAC
 GCTGGGAGTTTTATCTATTCTTTACATTGGATGCAAATGTATTACTCAAGAAGAGGCATTC
 GGTATCGAACCATAGATGAACATGATGCCATCATT**TAAG**GAAATCCATGGACCAAGGATGGA
 ATACAGATTGATGCTGCCCTATCAATTAATTTTGGTTTATTAATAGTTTAAACAATATTCT
 CTTTTTGAAAATAGTATAAACAGGCCATGCATATAATGTACAGTGTATTACGTAAATATGTA
 AAGATTCTTCAAGGTAACAAGGGTTTGGGTTTTGAAATAAACATCTGGATCTTATAGACCGT
 TCATACAATGGTTTTAGCAAGTTCATAGTAAGACAAACAAGTCCTATCTTTTTTTTTTTGGCT
 GGGGTGGGGGCATTGGTCACATATGACCAGTAATTGAAAGACGTCATCACTGAAAGACAGAA
 TGCCATCTGGGCATACAAATAAGAAGTTTGTACAGCACTCAGGATTTTGGGTATCTTTTGT
 AGCTCACATAAAGAAGTTTCAGTGCTTTTCAGAGCTGGATATATCTTAATTACTAATGCCACA
 CAGAAATTATACAATCAAACCTAGATCTGAAGCATAATTTAAGAAAAACATCAACATTTTTTG
 TGCTTTAAACTGTAGTAGTTGGTCTAGAAACAAAATACTCC

FIGURE 298

MGLGARGAWAALLLGTLQVLALLGAAHESAAMAASANIENSGLPHNSSANSTETLQHVP
SDH
TNETSNSTVKPPTSVASDSSNTTVTTMKPTAASNTTTPGMVSTNMTSTTLKSTPKTTSV
SQN
TSQISTSTMTVTHNSSVTSAASSVTITTTMHSEAKKGSKFDTGSFVGGIVLT
LGVL
SILYIG
CKMYYSRRGIRYRTIDEHDAII

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FIGURE 299

CAGCCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCCGG
TCGCGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCCAGCGATGGCGACCCTGTGGGGAGGC
CTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTTCGTGCCTGGCGCTTCCGTGCTGCTGCTGGC
GCAGCTGTCAGACGCCGCCAAGAATTTTCGAGGATGTCAGATGTAAATGTATCTGCCCTCCCT
ATAAAGAAAATTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTGTGATTGCCTT
CATGTTGTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTGTCTACGCTGTGA
ATGCAAATATGAAGAAAGAAGCTCTGTCACAATCAAGGTTACCATTATAATTTATCTCTCCA
TTTTGGGCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGAGCCCATACTGAAGAGG
CGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATATTGGGGATCACCAGCCTTT
TGCAAATGCACACGATGTGCTAGCCCGCTCCCGCAGTCGAGCCAACGTGCTGAACAAGGTAG
AATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCAGCGAAAGTCTGTCTTTGACCGG
CATGTTGTCCTCAGCTTAATTGGGAATTGAATTCAAGGTGACTAGAAAGAAACAGGCAGACAA
CTGGAAAGAACTGACTGGGTTTTGCTGGGTTTTCATTTTAATACCTTGTTGATTTACCAACT
GTTGCTGGAAGATTCAAACTGGAAGCAAAACTTGCTTGATTTTTTTTTCTTGTTAACGTA
ATAATAGAGACATTTTTTAAAGCACACAGCTCAAAGTCAGCCAATAAGTCTTTTCCTATTTG
TGACTTTTACTAATAAAAATAAATCTGCCTGTAAATTATCTTGAAGTCCTTTACCTGGAACA
AGCACTCTCTTTTTTACCACATAGTTTTAACTTGACTTTCAAGATAATTTTTCAGGGTTTTTG
TTGTTGTTGTTTTTTGTTTGTGTTTGGTGGGAGAGGGGAGGGATGCCTGGGAAGTGGTT
AACAACTTTTTTCAAGTCACTTTACTAAACAACTTTTGTAATAGACCTTACCTTCTATTT
TCGAGTTTCATTTATATTTTGCAGTGTAGCCAGCCTCATCAAAGAGCTGACTTACTCATTTG
ACTTTTGCAGTGAAGTATTATCTGGGTATCTGCTGTGTCTGCACTTCATGGTAAACGGGAT
CTAAAATGCCTGGTGGCTTTTCAAAAAAGCAGATTTTCTTCATGTACTGTGATGTCTGATG
CAATGCATCCTAGAACAACTGGCCATTTGCTAGTTTACTCTAAAGACTAAACATAGTCTTG
GTGTGTGTGGTCTTACTCATCTTCTAGTACCTTTAAGGACAAATCCTAAGGACTTGGACACT
TGCAATAAAGAAATTTTATTTTAAACCAAGCCTCCCTGGATTGATAATATATACACATTTG
TCAGCATTTCCGGTCGTGGTGAGAGGCAGCTGTTTGAGCTCCAATATGTGCAGCTTTGAACT
AGGGCTGGGGTTGTGGGTGCCTCTTCTGAAAGGTCTAACCATTATTGGATAACTGGCTTTTT
TCTTCCTATGTCCTCTTTGGAATGTAACAATAAAAATAATTTTTGAAACATCAA

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FIGURE 300

MATLWGGLRLGSLLSLSCLALSVLLLAQLSDAAKNFEDVRCKCICPPYKENS
GHYINKNIS
QKDCDCLHVVEPMPVRGPDVEAYCLRCECKYEERSSVTIKVTIIIIYLSILGLLLLYMVYLT
L
VEPILKRRLFGHAQLIQSDDDIGDHQPFANAHDVLARSRSRANVLNKVEYAQQRWKLQVQEQ
RKS VFDRHVLS

099161-11601
T09T1-13T650

FIGURE 301

GCACCTGCGACCACCGTGAGCAGTCATGGCGTACTCCACAGTGCAGAGAGTCGCTCTGGCTT
CTGGGCTTGTCTGGCTCTGTCTGCTGCTGCCCCAAGGCCTTCCTGTCCCGCGGGAAGCGG
CAGGAGCCGCCGCCGACACCTGAAGGAAAATTGGGCCGATTTCCACCTATGATGCATCATCA
CCAGGCACCCTCAGATGGCCAGACTCCTGGGGCTCGTTTTCCAGAGGTCTCACCTTGCCGAGG
CATTTGCAAAGGCCAAAGGATCAGGTGGAGGTGCTGGAGGAGGAGGTAGTGGAAGAGGTCTG
ATGGGGCAGATTATTCCAATCTACGGTTTTGGGATTTTTTTATATATACTGTACATTCTATT
TAAGGTAAGTAGAATCATCCTAATCATATTACATCAATTGAAAATCTAATATGGCGATAAAAA
TCATTGTCTACATTAAACTTCTTATAGTTCATAAAATTATTTCAAATCCATCATCTCTTTA
AATCCTGCCTCCTCTTCATGAGGTACTTAGGATAGCCATTATTTAGTTTCACATAAGAATG
TTTACTCAATGTTTAAGTGTGTTTTGCCCCAAAATTCACAATAACAAGGCAGAACTAGGACTT
GAACATGGATCTTTTGGTTCTTAATCCAGTGAGTGATACAATTCAATGCACTCCCCTGCCA

09941601.3160

Abstract

FIGURE 303

CGGCTCGAGTGCAGCTGTGGGGAGATTTTCAGTGCATTGCCTCCCCTGGGTGCTCTTCATCTT
 GGATTTGAAAGTTGAGAGCAGC**ATG**TTTTGCCCACTGAAACTCATCCTGCTGCCAGTGTTAC
 TGGATTATTCCTTGGGCCTGAATGACTTGAATGTTTCCCCGCCTGAGCTAACAGTCCATGTG
 GGTGATTCAGCTCTGATGGGATGTGTTTTCCAGAGCACAGAAGACAAATGTATATTCAAGAT
 AGACTGGACTCTGTCAACCAGGAGAGCACGCCAAGGACGAATATGTGCTATACTATTACTCCA
 ATCTCAGTGTGCCTATTGGGCGCTTCCAGAACCGCGTACACTTGATGGGGGACATCTTATGC
 AATGATGGCTCTCTCCTGCTCCAAGATGTGCAAGAGGCTGACCAGGGAACCTATATCTGTGA
 AATCCGCCTCAAAGGGGAGAGCCAGGTGTTCAAGAAGGCGGTGGTACTGCATGTGCTTCCAG
 AGGAGCCCCAAAGAGCTCATGGTCCATGTGGGTGGATTGATTGAGATGGGATGTGTTTTCCAG
 AGCACAGAAGTGAAACACGTGACCAAGGTAGAATGGATATTTTCAGGACGGCGCGCAAAGGA
 GGAGATTGTATTTCTTACTACCACAAACTCAGGATGTCTGTGGAGTACTCCAGAGCTGGG
 GCCACTTCCAGAATCGTGTGAACCTGGTGGGGGACATTTTCCGCAATGACGGTTCCATCATG
 CTTCAAGGAGTGAGGGAGTCAGATGGAGGAACTACACCTGCAGTATCCACCTAGGGAACCT
 GGTGTTCAAGAAAACCATTGTGCTGCATGTCAGCCCGGAAGAGCCTCGAACACTGGTGACCC
 CGGCAGCCCTGAGGCCTCTGGTCTTGGGTGGTAATCAGTTGGTGATCATTGTGGGAATTGTC
 TGTGCCACAATCCTGCTGCTCCCTGTTCTGATATTGATCGTGAAGAAGACCTGTGGAAATAA
 GAGTTCAGTGAATTCTACAGTCTTGGTGAAGAACACGAAGAAGACTAATCCAGAGATAAAAG
 AAAAACCCCTGCCATTTTGAAAGATGTGAAGGGGAGAAACACATTTACTCCCCAATAATTGTA
 CGGGAGGTGATCGAGGAAGAAGAACCAAGTGAAAAATCAGAGGCCACCTACATGACCATGCA
 CCCAGTTTGGCCTTCTCTGAGGTCAGATCGGAACAACCTCACTTGAAAAAAGTCAGGTGGGG
 GAATGCCAAAAACACAGCAAGCCTTT**TGAG**AAGAATGGAGAGTCCCTTCATCTCAGCAGCGG
 TGGAGACTCTCTCCTGTGTGTGTCTGGGCCACTCTACCAGTGATTTTCAGACTCCCGCTCTC
 CCAGCTGTCTCCTGTCTCATTGTTTGGTCAATACACTGAAGATGGAGAATTTGGAGCCTGG
 CAGAGAGACTGGACAGCTCTGGAGGAACAGGCCTGCTGAGGGGAGGGGAGCATGGACTTGGC
 CTCTGGAGTGGGACACTGGCCCTGGGAACCAGGCTGAGCTGAGTGGCCTCAAACCCCCGTT
 GGATCAGACCCTCCTGTGGGCAGGGTTCTTAGTGGATGAGTTACTGGGAAGAATCAGAGATA
 AAAACCAACCCAAATCAA

FIGURE 304

MFCPLKLILLPVLLDYSLGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKCI FKIDWTLSPG
EHAKDEYVLYYYSNLSVPIGRFQNRVHLMGDILCNDGSLLLQDVQEADQGT YICEIRLKGES
QVFKKAVVLHVLPEEPKELMVHVGG LIQMGCVFQSTEVKHVTKVEWIFSGRRAKEEIVFRYY
HKLRMSVEYSQSWG HFQNRVNLVGDIFRNDGSIMLQGVRES DGGNYTCS IHLGNLVFKKTIV
LHVSPEEPRTLVT PAALRPLVLGGNQLV IIVGIVCATILLLPVLILIVKKT CGNKSSVNSTV
LVKNTKKTNP EIKEKPCHFERCEGEKHIYSPIIVREVIEEEEPSEKSEATYMTMHPVWPSLR
SDRNN SLEKKSGGMPKTQQAF

T03T1 "T3T1560

FIGURE 305

CTATGAAGAAGCTTCCTGGAAAACAATAAGCAAAGGAAAACAAATGTGTCCCATCTCACATG
GTTCTACCCTACTAAAGACAGGAAGATCATAAACTGACAGATACTGAAATTGTAAGAGTTGG
AAACTACATTTTGC AAAGTCATTGAACTCTGAGCTCAGTTGCAGTACTCGGGAAGCC**ATGCA**
GGATGAAGATGGATACATCACCTTAAATATTAAAACTCGGAAACCAGCTCTCGTCTCCGTTG
GCCCTGCATCCTCCTCCTGGTGGCGTGTGATGGCTTTGATTCTGCTGATCCTGTGCGTGGGG
ATGGTTGTCGGGCTGGTGGCTCTGGGGATTTGGTCTGTCATGCAGCGCAATTACCTACAAGA
TGAGAATGAAAATCGCACAGGAACCTGCAACAATTAGCAAAGCGCTTCTGTCAATATGTGG
TAAAACAATCAGAACTAAAGGGCACTTTCAAAGGTCATAAATGCAGCCCCTGTGACACAAAC
TGGAGATATTATGGAGATAGCTGCTATGGGTTCTTCAGGCACAACCTAACATGGGAAGAGAG
TAAGCAGTACTGCACTGACATGAATGCTACTCTCCTGAAGATTGACAACCGGAACATTGTGG
AGTACATCAAAGCCAGGACTCATTTAATTCGTTGGGTCGGATTATCTCGCCAGAAGTCGAAT
GAGGTCTGGAAGTGGGAGGATGGCTCGGTTATCTCAGAAAATATGTTTGAGTTTTTGGGAAGA
TGGAAAAGGAAATATGAATTGTGCTTATTTTCATAATGGGAAAATGCACCCTACCTTCTGTG
AGAACAAACATTATTTAATGTGTGAGAGGAAGGCTGGCATGACCAAGGTGGACCAACTACCT
TAATGCAAAGAGGTGGACAGGATAACACAGATAAGGGCTTTATTGTACAATAAAAGATATGT
ATGAATGCATCAGTAGCTGAAAAAAAAAAAAA

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FIGURE 306

MQDEDGYITLNIKTRKPALVSVGPASSSWVRMALILLILCVGMVVGLVALGIWSVMQRNYL
QDENENRTGTLQQLAKRFCQYVVKQSELKGTFKGHKCSPCDTNWRYYGDSYGFRRHNLWE
ESKQYCTDMNATLLKIDNRNIVEYIKARTHLIRWVGLSRQKSNEVWKWEDGSVISENMFEFL
EDGKGNMNCAYFHNGKMHPTFCENKHLYLMCERKAGMTKVDQLP

TOP SECRET

FIGURE 308

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA28498

><subunit 1 of 1, 245 aa, 1 stop

><MW: 27564, pI: 10.18, NX(S/T): 1

MAAAIASSLIROKRQAREREKSNACKCVSSPSKGKTSCKDNKLNVF SRVKLFGSKKRRRRRP
EPQLKGIVTKLYSRQGYHLQLQADGTIDGTKDEDSTYTLFNLI PVGLRVVAIQGVQTKLYLA
MNSEGILYTSELF TPECKFKESVFENYYVTYSSMIYRQQQSGRGWYLGLNKEGEIMKGNHVK
KNKPAAHFLPKPLKVAMYKEPSLHDLTEFSRSGSGTPTKSRSVSGVLNGGKSMHNEST

N-glycosylation site.

amino acids 242-246

Glycosaminoglycan attachment site.

amino acids 165-169, 218-222

Tyrosine kinase phosphorylation site.

amino acids 93-100

N-myristoylation site.

amino acids 87-93, 231-237

ATP/GTP-binding site motif A (P-loop).

amino acids 231-239

HBGF/FGF family proteins

amino acids 78-94, 102-153

FIGURE 309

CCAGGATGGAGCTGGGGCCTGTATAGCCATATTATTGTTCTATGCTACTAGACATGGGGGGG
ACTTGGTGAAAAAGGTATTATCCAGCCAGAGGGTCTGGGAGCCCTGTCTTACTGAACCTGGG
CAACCTGGATATTCTGAGACATATTTTGGGGGGATTTCAGTGAAAAAAGTGGGGGATCCCCT
CCATTTAGAGTGTAGCAAAGGAAAAAACACCAAGGTTGGGTTTCCTTCCTGACATTGGCAGTG
CCCCAGTAGGGGTGGGATGAGCGAATATTCCCAAAGCTAAAGTCCCACACCCTGTAGATTAC
AAGAGTGGATTTGGCAGGAGTGTGCCCCAAAATACAGTGGAAGGTGCCTGAAGATATTTAA
ACCACGTCTTGAAAATTTAGTGGGTCTTGGCTTTGGGATAGGTGAAGTGAGGACAGACACTG
GAGAGGAGGGAAAGGGGACGTTTTCAATAGGAGGCAAACTCGAGGGTGGGATCCACTGAGG
AGTACATAGGCTGCTGGATCTGGTGGAGCCAGCACTGGGCCCACGGGTGGTAACTGGCTGCT
GTGGAGGGGGGTACGTGAGGGGGGGGTCTGGGGCTTATCCTCAGGTCCTGTGGGTGGGGCAG
CGAGTCGGGGCCTGAGCGTCAAGAGCATGCCCTAGTGAGCGGGCTCCTCTGGGGGAGCCCAG
CGCGCTCCGGGCGCCTGCCGGTTTGGGGGTGTCTCCTCCCGGGGCGCT**ATG**GCGGCGCTGGC
CAGTAGCCTGATCCGGCAGAAGCGGGAGGTCCGCGAGCCCGGGGGCAGCCGGCCGGTGTCGG
CGCAGCGGCGCGTGTGTCCCCGCGGCACCAAGTCCCTTTGCCAGAAGCAGCTCCTCATCCTG
CTGTCCAAGGTGCGACTGTGCGGGGGGCGGCCCCGCGCGGCCGACCGCGGCCCCGGAGCCTCA
GCTCAAAGGCATCGTCACCAAACCTGTTCTGCCGCCAGGGTTTCTACCTCCAGGCGAATCCCG
ACGGAAGCATCCAGGGCACCCCAGAGGATAACAGCTCCTTCACCCACTTCAACCTGATCCCT
GTGGGCCTCCGTGTGGTCACCATCCAGAGCGCCAAGCTGGGTCACTACATGGCCATGAATGC
TGAGGGACTGCTCTACAGTTCGCCGCATTTACAGCTGAGTGTGCTTTAAGGAGTGTGTCT
TTGAGAATTACTACGTCCTGTACGCCTCTGCTCTCTACCGCCAGCGTCGTTCTGGCCGGGCC
TGGTACCTCGGCCTGGACAAGGAGGGCCAGGTCATGAAGGGAAACCGAGTTAAGAAGACCAA
GGCAGCTGCCCACCTTTCTGCCCAAGCTCCTGGAGGTGGCCATGTACCAGGAGCCTTCTCTCC
ACAGTGTCCCGAGGCCTCCCCTTCCAGTCCCCCTGCCCCC**TGA**AATGTAGTCCCTGGACTG
GAGGTTCCCTGCACTCCCAGTGAGCCAGCCACCACCACAACCTGT

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FIGURE 310

MAALASSLIRQKREVREPGGSRPVSAQRRVCPRGTKSLCQKQLLILLSKVRLCGGRPARPDR
GPEPQLKGIVTKLFCRQGFYLAQNPDGSIQGTPEDTSSFTFENLIPVGLRVVTIQSAKLGHY
MAMNAEGLLYSSPHFTAECRFKECVFENYYVLYASALYRQRRSGRAWYLGLDKEGQVMKGNR
VKKTKAAAHFLPKLLEVAMYQEPSLHSVPEASPSSPPAP

Tyrosine kinase phosphorylation site:

amino acids 199-207

N-myristoylation sites:

amino acids 54-60, 89-95, 131-137

HBGF/FGF family signature:

amino acids 131-155

ATGGCCGCGGCCCATCGCTAGCGGCTTGATCCGCCAGAAGCGGCAGGCGCGGGAGCAGCACTG
GGACCGGCCGTCTGCCAGCAGGAGGCGGAGCAGCCCCAGCAAGAACCGCGGGCTCTGCAACG
GCAACCTGGTGGATATCTTCTCCAAAGTGCGCATCTTCGGCCTCAAGAAGCGCAGGTTGCGG
CGCCAAGATCCCCAGCTCAAGGGTATAGTGACCAGGTTATATTGCAGGCAAGGCTACTACTT
GCAAATGCACCCCGATGGAGCTCTCGATGGAACCAAGGATGACAGCACTAATTCTACACTCT
TCAACCTCATACCAGTGGGACTACGTGTTGTTGCCATCCAGGGAGTGAAAACAGGGTTGTAT
ATAGCCATGAATGGAGAAGGTTACCTCTACCCATCAGAACTTTTTACCCCTGAATGCAAGTT
TAAAGAATCTGTTTTTGAAAATTATTATGTAATCTACTCATCCATGTTGTACAGACAACAGG
AATCTGGTAGAGCCTGGTTTTTGGGATTAAATAAGGAAGGGCAAGCTATGAAAGGGAACAGA
GTAAAGAAAACCAAACCAGCAGCTCATTTTCTACCCAAGCCATTGGAAGTTGCCATGTACCG
AGAACCATCTTTGCATGATGTTGGGGAAACGGTCCCGAAGCCTGGGGTGACGCCAAGTAAAA
GCACAAGTGCGTCTGCAATAATGAATGGAGGCAAACCAGTCAACAAGAGTAAGACAACAT**TAG**

FIGURE 312

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA28503
```

><subunit 1 of 1, 247 aa, 1 stop

><MW: 27702, pI: 10.36, NX(S/T): 2

MAAAIASGLIRQKRQAREQHWDRPSASRRRSSPSKNRGLCNGNLVDIFSKVRI FGLKKRRLR
RQDPQLKGI VTRLYCRQGYLQMHDPGALDGT KDDSTNSTLFNLI PVGLRVVAIQGVKTGLY
IAMNGEGYLYPSELFTPECKFKESVFENYYVIYSSMLYRQQESGRAWFLGLNKEGQAMKGNR
VKKTKPAAHFLPKPLEVAMYREPSLHDVGETVPKPGVTPSKSTSASAIMNGGKPVNKS KTT

N-glycosylation site.

amino acids 100-104, 242-246

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 28-32, 29-33

Tyrosine kinase phosphorylation site.

amino acids 199-207

N-myristoylation site.

amino acids 38-44, 89-95, 118-124, 122-128, 222-228

HBGF/FGF family proteins.

amino acids 104-155, 171-198

FIGURE 313

GGGGAGAGGAATTGACCATGTAAAAGGAGACTTTTTTTTTTGGTGGTGGTGGCTGTTGGGTGCCTTGCAAAAAT
GAAGGATGCAGGACGCAGCTTTCTCCTGGAACCGAACGCAATGGATAAACTGATTGTGCAAGAGAGAAGGAAGA
ACGAAGCTTTTTCTGTGAGCCCTGGATCTTAACACAAATGTGTATATGTGCACACAGGGAGCATTCAAGAATG
AAATAAACAGAGTTAGACCCGCGGGGTTGGTGTGTTCTGACATAAATAAATAATCTTAAAGCAGCTGTTCCC
CTCCCCACCCCCAAAAAAGGATGATTGGAAATGAAGAACCGAGGATTCACAAAGAAAAAAGTATGTTCAATTT
TTCTCTATAAAGGAGAAAGTGAGCCAAGGAGATATTTTTGGAATGAAAAGTTTGGGGCTTTTTTAGTAAAGTAA
AGAAGTGGTGTGGTGGTGTTCCTTTCTTTTTGAATTTCCCACAAGAGGAGAGGAAATTAATAATACATCTGC
AAAGAAATTTAGAGAAGAAAAGTTGACCGCGCAGATTGAGGCATTGATTGGGGGAGAGAAAACAGCAGAGCA
CAGTTGGATTTGTGCCTATGTTGACTAAAATTGACGGATAATTGCAGTTGGATTTTTCTTCATCAACCTCCTTT
TTTTTAAATTTTTATTCTTTTGGTATCAAGATCATGCGTTTTCTCTTGTCTTAACCACTGGATTTCCATCT
GGATGTTGCTGTGATCAGTCTGAAATACAACTGTTGAATTCAGAAGGACCAACACCAGATAAAATTATGAATG
TTGAACAAGATGACCTTACATCCACAGCAGATAATGATAGGTCCTAGGTTTAACAGGGCCCTATTTGACCCCT
GCTTGTGGTGTGCTGCTGGCTCTTCAACTTCTTGTGGTGGCTGGTCTGGTGCGGGCTCAGACCTGCCCTCTGTGT
GCTCCTGCAGCAACCAGTTGAGCAAGGTGATTTGTGTTGCGAAAACCTGCGTGAGGTTCCGGATGGCATCTCC
ACCAACACACGGCTGCTGAACCTCCATGAGAACCAATCCAGATCATCAAAGTGAACAGCTTCAAGCACTTGAG
GCACTTGGAATCCTACAGTTGAGTAGGAACCATATCAGAACCATTGAAATGGGGCTTTCAATGGTCTGGCGA
ACCTCAACACTCTGGAACCTTTGACAATCGTCTTACTACCATCCCGAATGGAGCTTTGTATACCTGTCTAAA
CTGAAGGAGCTCTGGTTGCGAAACAACCCCATGAAAGCATCCCTTCTTATGCTTTTAACAGAATTCCTTCTTT
GCGCCGACTAGACTTAGGGGAATTGAAAAGACTTTCATACATCTCAGAAGGTGCCTTTGAAGGTCTGTCCAAT
TGAGGTATTTGAACCTTGCCATGTGCAACCTTCGGGAAATCCCTAACCTCACACCGCTCATAAAAGTAGATGAG
CTGGATCTTTCTGGGAATCATTTATCTGCCATCAGGCCTGGCTCTTCCAGGGTTTGATGCACCTTCAAAAAT
GTGGATGATACAGTCCAGATTCAAGTGATTGAACGGAATGCCTTTGACAACCTTCAGTCACTAGTGGAGATCA
ACCTGGCACACAATAATCTAACATTACTGCCTCATGACCTCTTCACTCCCTTGATCATCTAGAGCGGATACAT
TTACATCACAAACCTTGGAACGTGTAACGTGTGACATACTGTGGCTCAGCTGGTGGATAAAAGACATGGCCCCCTC
GAACACAGCTTGTTGTGCCCCGTGTAACACTCCTCCCAATCTAAAGGGGAGGTACATTGGAGAGCTCGACCAGA
ATTACTTCACATGCTATGCTCCGGTGATTGTGGAGCCCCCTGCAGACCTCAATGTCACTGAAGGCATGGCAGCT
GAGCTGAAATGTGCGGCCTCCACATCCCTGACATCTGTATCTTGGATTACTCCAAATGGAACAGTCATGACACA
TGGGGCGTACAAAGTGCAGATAGCTGTGCTCAGTGATGGTACGTTAAATTTACAAATGTAACGTGTGCAAGATA
CAGGCATGTACACATGTATGGTGAGTAATTCGGTTGGGAATACTACTGCTTCAGCCACCCTGAATGTTACTGCA
GCAACCACTACTCCTTTCTCTTACTTTTTCAACCGTCACAGTAGAGACTATGGAACCGTCTCAGGATGAGGCACG
GACCACAGATAACAATGTGGGTCCCACTCCAGTGGTGCAGTGGGAGACCACCAATGTGACCACCTCTCTCACAC
CACAGAGCACAAGGTGACAGAGAAAACCTTCACCATCCAGTGACTGATATAAACAGTGGGATCCAGGAATT
GATGAGGTCATGAAGACTACCAAAATCATCATTGGGTGTTTTGTGGCCATCACACTCATGGCTGCAGTGATGCT
GGTCATTTTCTACAAGATGAGGAAGCAGCACCATCGGCAAAACCATCACGCCCCAACAAAGGACTGTTGAAATTA
TTAATGTGGATGATGAGATTACGGGAGACACACCCATGGAAGCCACCTGCCATGCCTGCTATCGAGCATGAG
CACCTAAATCACTATAACTCATACAAATCTCCCTTCAACCACACAACAACAGTTAACACAATAAATTCAATACA
CAGTTCAGTGATGAACCGTTATTGATCCGAATGAACCTTAAAGACAATGTACAAGAGACTCAAATCTAAACA
TTTACAGAGTTACAAAAAACAAACAATCAAAAAAAGACAGTTTATTAAAAATGACACAAATGACTGGGCTAA
ATCTACTGTTTCAAAAAAGTGTCTTTACAAAAAACAAGAAAGAAATTTATTTATTAATAATTCTATTG
TGATCTAAAGCAGACAAAAA

FIGURE 314

MLNKMTLHPQQIMIGPRFNRALFDPLLVLALLQLLVVAGLVRAQTCPSVCSCSNQFSKVIC
 VRKNLREVPDGISTNTRLLNLHENQIQIIVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLA
 NLNTLELFDNRLTTIPNGAFVYLSKLELWLRNPNIESIPSYAFNRIPSLRRLDLGELKRLS
 YISEGAFEGLSNRLRYLNLAMCNLREIPNLTPLIKLDELDSLGNHLSAIRPGSFQGLMHLQKL
 WMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLLHNPWNCNCDIL
 WLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTEGMAAE
 LKCRASSTLSVSWITPNGTVMTHGAYKVRIAVLSDGTNLNFTNVTQDTGMYTCMVNSVGN
 TTASATLNVTAATTTTPFSYFSTVTVETMEPSQDEARTTDNNVGPTPVVDWETTNVTTSLTPQ
 STRSTEKFTTIPVTDINSGIPGIDEVMKTTKIIIGCFVAITLMAAVMLVIFYKMRKQHRQN
 HHAPTRTVEIINVDDDEITGDTPMESHLPMPAIEHEHLNHYSYKSPFNHTTTVNTINSIHSS
 VHEPLLIRMNSKDNVQETQI

Signal sequence:

amino acids 1-44

Transmembrane domain:

amino acids 523-543

N-glycosylation site.

amino acids 278-282, 364-368, 390-394, 412-416, 415-419,
 434-438, 442-446, 488-492, 606-610

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 183-187

Casein kinase II phosphorylation site.

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

N-myristoylation site.

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,
 391-397, 422-428, 433-439, 531-537

GCCTCGGGAGCCCATCTGCCCCAGGGGCACGGGGCGCGGGGGCGGCTCCCGCCCGGCACAT
GGCTGCAGCCACCTCGCGGCACCCCGAGGCGCCGCGCCAGCTCGCCCGAGGTCCGTCCGA
GGCGCCCGGCCGCCCCGGAGCCAAGCAGCAACTGAGCGGGGAAGCGCCCGCGTCCGGGGATC
GGG**ATG**TCCCTCCTCCTTCTCCTCCTTGCTAGTTTCTTACTATGTTGGAACCTTGGGGACTCA
CACTGAGATCAAGAGAGTGGCAGAGGAAAAGGTCACCTTTGCCCTGCCACCATCAACTGGGGC
TTCCAGAAAAAGACACTCTGGATATTGAATGGCTGCTCACCGATAATGAAGGGAACCAAAAA
GTGGTGATCACTTACTCCAGTCGTCATGTCTACAATAACTTGACTGAGGAACAGAAGGGCCG
AGTGGCCTTTGCTTCCAATTTCCCTGGCAGGAGATGCCTCCTTGCGAGATTGAACCTCTGAAGC
CCAGTGATGAGGGCCGGTACACCTGTAAGGTTAAGAATTCAGGGCGCTACGTGTGGAGCCAT
GTCATCTTAAAGTCTTAGTGAGACCATCCAAGCCCCAAGTGTGAGTTGGAAGGAGAGCTGAC
AGAAGGAAGTGACCTGACTTTGCAGTGAGTGCATCCTCTGGCACAGAGCCCATTGTGTATT
ACTGGCAGCGAATCCGAGAGAAAGAGGGAGAGGATGAACGTCTGCCTCCCAAATCTAGGATT
GACTACAACCACCTTGACGAGTTCTGCTGCGAGAATCTTACCATGTCCTACTCTGGACTGTA
CCAGTGCCACAGCAGGCAACGAAGCTGGGAAGGAAAGCTGTGTGGTGCGAGTAAGTGTACAGT
ATGTACAAGCATCGGCATGGTTGCAGGAGCAGTGACAGGCATAGTGGCTGGAGCCCTGCTG
ATTTTCCTCTTGGTGTTGGCTGCTAATCCGAAGGAAAGACAAAGAAAGATATGAGGAAGAAGA
GAGACCTAATGAAATTCGAGAAGATGCTGAAGCTCCAAAAGCCCGTCTTGTGAAACCCAGCT
CCTCTTCCTCAGGCTCTCGGAGCTCACGCTCTGTTTCTTCCTCCACTCGCTCCACAGCAAAT
AGTGCCTCACGCAGCCAGCGGACACTGTCAACTGACGCAGCACCCCAGCCAGGGCTGGCCAC
CCAGGCATACAGCCTAGTGGGGCCAGAGGTGAGAGGTTCTGAACCAAAGAAAGTCCACCATG
CTAATCTGACCAAAGCAGAAACCACACCCAGCATGATCCCCAGCCAGAGCAGAGCCTTCCAA
ACGGT**CTGA**ATTACAATGGACTTGACTCCACGCTTTCTTAGGAGTCAGGGTCTTTGGACTC
TTCTCGTCATTGGAGCTCAAGTCACCAGCCACACAACCAGATGAGAGGTCATCTAAGTAGCA
GTGAGCATTGCACGGAACAGATTAGATGAGCATTTTCTTTATACAATACCAAACAAGCAAA
AGGATGTAAGCTGATTATCTGTAAAAAGGCATCTTATTGTGCCTTTAGACCAGAGTAAGGG
AAAGCAGGAGTCCAAATCTATTTGTTGACCAGGACCTGTGGTGAGAAGGTTGGGGAAAGGTG
AGGTGAATATACCTAAAACCTTTAATGTGGGATATTTGTATCAGTGCTTTGATTCACAATT
TTCAAGAGGAAATGGGATGCTGTTTGTAATTTTCTATGCATTTCTGCAAACCTTATTGGATT
ATTAGTTATTCAGACAGTCAAGCAGAACCCACAGCCTTATTACACCTGTCTACACCATGTAC
TGAGCTAACCACTTCTAAGAAACTCCAAAAAAGGAAACATGTGTCTTCTATTCTGACTTAAC
TTCATTTGTCTATAAGGTTTGGATATTAATTTCAAGGGGAGTTGAAATAGTGGGAGATGGAGA
AGAGTGAATGAGTTTCTCCCACTCTATACTAATCTCACTATTTGTATTGAGCCCCAAAATAAC
TATGAAAGGAGACAAAAATTTGTGACAAAGGATTGTGAAGAGCTTTCCATCTTCATGATGTT
ATGAGGATTGTTGACAAACATTAGAAATATATAATGGAGCAATTGTGGATTTCCCCTCAAAT
CAGATGCCTCTAAGGACTTTCTGCTAGATATTTCTGGAAGGAGAAAATACAACATGTCATT
TATCAACGTCCTTAGAAAGAATTCTTCTAGAGAAAAAGGGATCTAGGAATGCTGAAAGATT
CCCAACATACCATTTATAGTCTCTTCTTTCTGAGAAAAATGTGAAACCAGAATTGCAAGACTGG
GTGGACTAGAAAGGGAGATTAGATCAGTTTTCTCTTAATATGTCAAGGAAGGTAGCCGGGCA
TGGTGCCAGGCACCTGTAGGAAAATCCAGCAGGTGGAGGTTGCAGTGAGCCGAGATTATGCC
ATTGCACTCCAGCCTGGGTGACAGAGCGGGACTCCGTCTC

316/330

FIGURE 316

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45419

><subunit 1 of 1, 373 aa, 1 stop

><MW: 41281, pI: 8.33, NX(S/T): 3

MSLLLLLLLLVSYYVGTLGTHTEIKRVAEEKVTLPCHHQLGLPEKDTLDIEWLLTDNEGNQKV
VITYSSRHVYNNLTTEEQKGRVAFASNFLAGDASLQIEPLKPSDEGRYTCKVKNSGRYVWSHV
ILKVLVRPSKPKCELEGELTEGSDLTLCESSTGTEPIVYYWQRIREKEGEDERLPPKSRID
YNHPGRVLLQNLMTSYSGLYQCTAGNEAGKESCVVRVTVQYVQSIGMVAGAVTGIVAGALLI
FLLVWLLIRRKDKERYEEEEERPNEIREDAEAPKARLVKPSSSSSSGSRSSRSGSSSTRSTANS
ASRSQRTLSTDAAPQPGLATQAYSLVGPEVRGSEPKKVHHANLTKAETTPSMIPSQSRAFQTV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 232-251

Transmembrane domain

FIGURE 317

CGCGAGGCGCGGGGAGCCTGGGACCAGGAGCGAGAGCCGCCTACCTGCAGCCGCGCCACGGCACGGCAGGCCA
 CC**ATG**GCGCTCCTGCTGTGCTTCGTGCTCCTGTGCGGAGTAGTGGATTTCCGCCAGAAAGTTTGAGTATCACTACT
 CCTGAAGAGATGATTGAAAAAGCCAAAGGGGAAACTGCCTATCTGCCATGCAAATTTACGCTTAGTCCCGAAGA
 CCAGGGACCGCTGGACATCGAGTGGCTGATATCACCAGCTGATAATCAGAAGGTGGATCAAGTGATTATTTTAT
 ATTCTGGAGACAAAATTTATGATGACTACTATCCAGATCTGAAAGGCCGAGTACATTTTACGAGTAATGATCTC
 AAATCTGGTGATGCATCAATAAATGTAACGAATTTACAACCTGTGAGATATTTGGCACATATCAGTGCAAAGTGAA
 AAAAGCTCCTGGTGTTGCAAATAAGAAGATTCATCTGGTAGTTCTTGTTAAGCCTTCAGGTGCGAGATGTTACG
 TTGATGGATCTGAAGAAATTGGAAGTGACTTTAAGATAAAATGTGAACCAAAGAAGGTTCACTTCCATTACAG
 TATGAGTGGCAAAAATTTGTCTGACTCACAGAAAATGCCCACTTCATGGTTAGCAGAAATGACTTCATCTGTTAT
 ATCTGTAAAAAATGCCTCTTCTGAGTACTCTGGGACATACAGCTGTACAGTCAGAAACAGAGTGGGCTCTGATC
 AGTGCCTGTTGCGTCTAAACGTTGTCCCTCCTTCAAATAAAGCTGGACTAATTGCAGGAGCCATTATAGGAACT
 TTGCTTGCTCTAGCGCTCATTGGTCTTATCATCTTTTGCTGTGCTGTAAGCGCAGAGAAGAAAAATATGAAAA
 GGAAGTTCATCACGATATCAGGGAAGATGTGCCACCTCCAAAGAGCCGTACGTCCACTGCCAGAAGCTACATCG
 GCAGTAATCATTATCCCTGGGGTCCATGTCTCCTTCCAACATGGAAGGATATTCCAAGACTCAGTATAACCAA
 GTACCAAGTGAAGACTTTGAACGCACCTCCTCAGAGTCCGACTCTCCACCTGCTAAGTTCAAGTACCCTTACAA
 GACTGATGGAATTACAGTTGTAT**TAA**ATATGGACTACTGAAGAATCTGAAGTATTGTATTATTTGACTTTATTTT
 AGGCCTCTAGTAAAGACTTAAATGTTTTTAAAAAAGCACAAAGGCACAGAGATTAGAGCAGCTGTAAGAACAC
 ATCTACTTTTATGCAATGGCATTAGACATGTAAGTCAGATGTGATGTCAAATTTAGTACGAGCCAAATTCCTTGT
 TAAAAAACCTATGTATAGTGACACTGATAGTTAAAAGATGTTTTATTATATTTTCAATAACTACCACTAACAA
 ATTTTAACTTTTTCATATGCATATTCTGATATGTGGTCTTTTAGGAAAAGTATGGTTAATAGTTGATTTTCAA
 AGGAAATTTTAAATTTCTTACGTTCTGTTTAAATGTTTTTGCTATTTAGTTAAATACATGTAAGGGAAATACCCG
 TTCTTTTCCCTTTTATGCACACAACAGAAACACGCGTTGTGATGCCTCAAACCTATTTTATTTGCAACTACA
 TGATTTTACACAATTCTCTTAAACAACGACATAAAATAGATTTCTTGTATATAAATAACTTACATACGCTCCA
 TAAAGTAAATTCTCAAAGGTGCTAGAACAATCGTCCACTTCTACAGTGTTCTCGTATCCAACAGAGTTGATGC
 ACAATATATAAATACTCAAGTCCAATATTAAAACTTAGGCACCTGACTAACTTTAATAAAATTTCTCAAACCTA
 TATCAATATCTAAAGTGACATATATTTTTTAAGAAAGATTATTTCTCAATAACTTCTATAAAAAATAAGTTTGATGG
 TTTGGCCCATCTAACTTCACTACTATTAGTAAGAATTTTAACTTTTAAATGTGTAGTAAGGTTTATTTCTACCTT
 TTTCTCAACATGACACCAACACAATCAAAAACGAAGTTAGTGAGGTGCTAACATGTGAGGATTAATCCAGTGAT
 TCCGGTCACAATGCATTCCAGGAGGAGGTACCCATGTCACTGGAATTGGGCGATATGGTTTATTTTTTCTTCCC
 TGATTTGGATAACCAAATGGAACAGGAGGAGGATAGTGATTCTGATGGCCATTCCCTCGATACATTCCCTGGCTT
 TTTTCTGGGCAAAGGTGCCACATTGGAAGAGGTGGAATATAAGTTCTGAAATCTGTAGGGAAGAGAACACAT
 TAAGTTAATTCAAAGGAAAAAATCATCATCTATGTTCCAGATTTCTCATTAAGACAAAGTTACCCACAACACT
 GAGATCACATCTAAGTGACACTCCTATTGTGAGGTCTAAATACATTAAAAACCTCATGTGTAATAGGCGTATAA
 TGTATAACAGGTGACCAATGTTTTCTGAATGCATAAAGAAATGAATAAACTCAAACACAGTACTTCCCTAAACAA
 CTTCAACCAAAAAAGACCAAAACATGGAACGAATGGAAGCTTGTAAGGACATGCTTGTTTTAGTCCAGTGGTTT
 CCACAGCTGGCTAAGCCAGGAGTCACTTGGAGGCTTTTAAATACAAAACATTGGAGCTGGAGGCCATTATCCTT
 AGCAAACCTAATGCAGAAACAGAAAATCAACTACCGCATGTTCTCACTTATAAGTGGGAGGTAATGATAAGAACT
 TATGAACACAAAGAAGGAAACAATAGACATTGGAGTCTATTTGAGAGGGGAGGTGGGAGAAGGAAAAGGAGCA
 GAAAAGATAACTATTGAGTACTGCCTTCACACCTGGGTGATGAAATAATATGTACAACAAATCCCTGTGACACA
 TGTTTACCTATGGAACAAACCTTCATGTGTATCCCTAAACCTAAAAATAAAAGTTAAAAAARAAAAA
 AA
 AAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 318

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA82361

><subunit 1 of 1, 352 aa, 1 stop

><MW: 38938, pI: 7.86, NX(S/T): 3

MALLLCFVLLCGVVDFARSLSITTPPEEMIEKAKGETAYLPCKFTLSPEDQGPLDIEWLISPA
DNQKVDQVIILYSGDKIYDDYYPDLKGRVHFTSNDLKSGDASINVTNLQLSDIGTYQCKVKK
APGVANKKIHLLVVLVKPSGARCIVDGSSEEIGSDFKIKCEPKEGSLPLQYEWQKLSDSQKMPT
SWLAEMTSSVISVKNASSEYSGTYCTVRNRVGSQCLLRNLNVPPSNKAGLIAGAIIGTLL
ALALIGLIIFCCRKKRREEKYEKEVHHDIREDVPPPKSRTSTARSYIGSNHSSLGSMSPSNM
EGYSKTQYNQVPSEDFERTPQSPTLPPAKFKYPYKTDGITVV

Signal sequence.

amino acids 1-19

Transmembrane domain:

amino acids 236-257

N-glycosylation sites.

amino acids 106-110, 201-205, 298-302

Tyrosine kinase phosphorylation sites.

amino acids 31-39, 78-85, 262-270

N-myristoylation sites.

amino acids 116-122, 208-214, 219-225, 237-243, 241-247,
245-251, 296-302

Myelin P0 protein.

amino acids 96-125

FIGURE 319

TGAAATGACTTCCACGGCTGGGACGGGAACCTTCCACCCACAGCTATGCCTCTGATTGGTGA
 ATGGTGAAGGTGCCTGTCTAACTTTTCTGTAAAAAGAACCAGCTGCCTCCAGGCAGCCAGCC
 CTCAAGCATCACTTACAGGACCAGAGGGACAAGACATGACTGTGATGAGGAGCTGCTTTCGC
 CAATTTAACACCAAGAAGAATTGAGGCTGCTTGGGAGGAAGGCCAGGAGGAACACGAGACTG
 AGAGATGAAATTTTCAACAGAGGCTGCAAAGCCTGTGGACTTTAGCCAGACCCTTCTGCCCTC
 CTTTGCTGGCGACAGCCTCTCAAATGCAGATGGTTGTGCTCCCTTGCCTGGGTTTTACCCTG
 CTTCTCTGGAGCCAGGTATCAGGGGCCAGGGCCAAGAATTCCACTTTGGGCCCTGCCAAGT
 GAAGGGGGTTGTTCCCCAGAACTGTGGGAAGCCTTCTGGGCTGTGAAAGACACTATGCAAG
 CTCAGGATAACATCACGAGTGCCCCGGCTGCTGCAGCAGGAGGTTCTGCAGAACGTCTCGGAT
 GCTGAGAGCTGTTACCTTGTCCACACCCTGCTGGAGTTCTACTTGAAAAGTGTTCCTCAAAAA
 CCACCACAATAGAACAGTTGAAGTCAGGACTCTGAAGTCATTCTCTACTCTGGCCAACAAC
 TTGTTCTCATCGTGTCACAACTGCAACCCAGTCAAGAAAATGAGATGTTTTCCATCAGAGAC
 AGTGCACACAGGCGGTTTTCTGCTATTCCGGAGAGCATTCAAACAGTTGGACGTAGAAGCAGC
 TCTGACCAAAGCCCTTGGGGAAGTGGACATTCTTCTGACCTGGATGCAGAAATTCTACAAGC
 TCTGAATGTCTAGACCAGGACCTCCCTCCCCCTGGCACTGGTTTTGTTCCCTGTGTCAATTTCA
 AACAGTCTCCCTTCCTATGCTGTTCACTGGACACTTCACGCCCTTGGCCATGGGTCCCATT
 TTGGCCCAGGATTATTGTCAAAGAAGTCATTCTTTAAGCAGCGCCAGTGACAGTCAGGGAAG
 GTGCCTCTGGATGCTGTGAAGAGTCTACAGAGAAGATTCTTGTATTTATTACAACCTCTATTT
 AATTAATGTCAGTATTTCAACTGAAGTTCTATTTATTTGTGAGACTGTAAGTTACATGAAGG
 CAGCAGAATATTGTGCCCCATGCTTCTTTACCCCTCACAATCCTTGCCACAGTGTGGGGCAG
 TGGATGGGTGCTTAGTAAGTACTTAATAAACTGTGGTGCTTTTTTTTGGCCTGTCTTTGGATT
 GTTAAAAAACAGAGAGGGATGCTTGGATGTAAACTGAACTTCAGAGCATGAAAATCACACT
 GTCTTCTGATATCTGCAGGGACAGAGCATTGGGGTGGGGGTAAGGTGCATCTGTTTGAAAAG
 TAAACGATAAAATGTGGATTAAAGTGCCAGCACAAAGCAGATCCTCAATAAACATTTCAAT
 TCCCACCCACACTCGCCAGCTCACCCCATCATCCCTTTCCCTTGGTGCCCTCCTTTTTTTTT
 TATCCTAGTCATTCTTCCCTAATCTTCCACTTGAGTGTCAAGCTGACCTTGCTGATGGTGAC
 ATTGACCTGGATGTACTATCCAATCTGTGATGACATTCCCTGCTAATAAAAGACAACATAA
 CTCCAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 320

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA88002

><subunit 1 of 1, 206 aa, 1 stop

><MW: 23799, pI: 9.12, NX(S/T): 3

MNFQQRLQSLWTLARPFPCPLLATASQMOMVVLPCLGFTLLLWSQVSGAQGQEFHFGPCQVK
GVVPQKLWEAFWAVKDTMQAQDNITSARLLQQEVLQNVSDAESCYLEVHTLLEFYLKTVFKNH
HNRTVEVRTLKSFSTLANNFVLIVSQLQPSQENEMFSIRDSAHRRFLLFRRAFKQLDVEAAL
TKALGEVDILLTWMQKFYKL

Signal sequence:

amino acids 1-42

N-glycosylation sites.

amino acids 85-89, 99-103, 126-130

FIGURE 321

AAGGAGCAGCCCGCAAGCACCAAGTGAGAGGCATGAAGTTACAGTGTGTTTCCCTTTGGCTC
CTGGGTACAATACTGATATTGTGCTCAGTAGACAACCACGGTCTCAGGAGATGTCTGATTTT
CACAGACATGCACCATATAGAAGAGAGTTTCCAAGAAATCAAAGAGCCATCCAAGCTAAGG
ACACCTTCCCAAATGTCACATCCTGTCCACATTGGAGACTCTGCAGATCATTAAGCCCTTA
GATGTGTGCTGCGTGACCAAGAACCTCCTGGCGTTCTACGTGGACAGGGTGTTCAAGGATCA
TCAGGAGCCAAACCCCAAATCTTGAGAAAAATCAGCAGCATTGCCAACTCTTTCCTCTACA
TGCAGAAAATCTGCGGCAATGTCAGGAACAGAGGCAGTGTCACTGCAGGCAGGAAGCCACC
AATGCCACCAGAGTCATCCATGACAACTATGATCAGCTGGAGGTCCACGCTGCTGCCATTAA
ATCCCTGGGAGAGCTCGACGTCTTCTAGCCTGGATTAATAAGAATCATGAAGTAATGTTCT
CAGCTTGATGACAAGGAACCTGTATAGTGATCCAGGGATGAACACCCCCTGTGCGGTTTACT
GTGGGAGACAGCCCACCTTGAAGGGGAAGGAGATGGGGAAGGCCCTTGCAGCTGAAAGTCC
CACTGGCTGGCCTCAGGCTGTCTTATTCCGCTTGAAAATAGGCAAAAAGTCTACTGTGGTAT
TTGTAATAAACTCTATCTGCTGAAAGGGCCTGCAGGCCATCCTGGGAGTAAAGGGCTGCCTT
CCCATCTAATTTATTGTAAAGTCATATAGTCCATGTCTGTGATGTGAGCCAAGTGATATCCT
GTAGTACACATTGTACTGAGTGGTTTTTCTGAATAAATTCCATATTTTACCTATGA

FIGURE 322

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></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA92282
```

><subunit 1 of 1, 177 aa, 1 stop

><MW: 20452, pI: 8.00, NX(S/T): 2

MKLCVSLWLLGTILILCSVDNHGLRRCLISTDMHHIEESFOEIKRAIQAKDTFPNVTILST

LETLQIIKPLDVCCVTKNLLAFYVDRVFKDHQEPNPKILRKISSIANSFLYMQKTLRQCQEQ

RQCHCRQEATNATRVIHNDYDQLEVHAAAIKSLGELDVFLAWINKNHEVMFSA

Signal sequence:

amino acids 1-18

N-glycosylation sites.

amino acids 56-60, 135-139

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 102-106

N-myristoylation site.

amino acids 24-30

Actinin-type actin-binding domain signature 1.

amino acids 159-169

FIGURE 323

CCCGTGCCAAGAGTGACGTAAGTACCGCCTATAGAGTCTATAGGCCCACTTGGCTTCGTTAG
AACGCGGCTACAATTAATACATAACCTTATGTATCATACACATACGATTTAGGTGACACTAT
AGAATAACATCCACTTTGCCTTTCTCTCCACAGGTGTCCACTCCCAGGTCCAACTGCACCTC
GGTTCTATCGATAATCTCAGCACCCAGCCACTCAGAGCAGGGCACGATGTTGGGGGCCCCGCT
CAGGCTCTGGGTCTGTGCCTTGTGCAGCGTCTGCAGCATGAGCGTCCTCAGAGCCTATCCCA
ATGCCTCCCCACTGCTCGGCTCCAGCTGGGGTGGCCTGATCCACCTGTACACAGCCACAGCC
AGGAACAGCTACCACCTGCAGATCCACAAGAATGGCCATGTGGATGGCGCACCCCATCAGAC
CATCTACAGTGCCCTGATGATCAGATCAGAGGATGCTGGCTTTGTGGTGATTACAGGTGTGA
TGAGCAGAAGATACCTCTGCATGGATTTTCTAGAGGCAACATTTTTGGATCACACTATTTTCGAC
CCGGAGAACTGCAGGTTCCAACACCAGACGCTGGAAAACGGGTACGACGCTTACCACTCTCC
TCAGTATCACTTCCTGGTCAGTCTGGGCCGGGCGAAGAGAGCCTTCCTGCCAGGCATGAACC
CACCCCCGTACTCCCAGTTCCTGTCCCGGAGGAACGAGATCCCCCTAATTCATTCAACACC
CCCATACCACGGCGGCACACCCGGAGCGCCGAGGACGACTCGGAGCGGGACCCCTGAACGT
GCTGAAGCCCCGGGCCCCGGATGACCCCGGCCCCGGCCTCCTGTTTACAGGAGCTCCCGAGCG
CCGAGGACAACAGCCCGATGGCCAGTGACCCATTAGGGGTGGTCAGGGGCGGTTCGAGTGAAC
ACGCACGCTGGGGGAACGGGCCCCGGAAGGCTGCCGCCCTTCGCCAAGTTCATCTAGGGTCTG
CTGG

099181.11604

FIGURE 324

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA142238

><subunit 1 of 1, 251 aa, 1 stop

><MW: 27954, pI: 9.22, NX(S/T): 1

MLGARLRLWVCALCSVCSMSVLRAYPNASPLLGSWSGGLIHLYTATARN SYHLQIHKN GHVD
 GAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNI FGSHYFDPENCRFQHQTLENGY
 DVIHSPQYHFLVSLGRAKRAFLPGMNPPYPYSQFLSRNEIPLIHFNTPIPRRHTRSAEDDSE
 RDPLNLVKPRARMT PAPASCSQELPSAEDNSPMASDPLGVVRGGRVNT HAGGTGPEGCRPFA
 KFI

Important features of the protein:

Signal peptide:

amino acids 1-24

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 175-179

N-myristoylation site.

amino acids 33-39, 100-106, 225-231, 229-235

HBGF/FGF family proteins

amino acids 73-124

FIGURE 325

GGAAAAGGTACCCGCGAGAGACAGCCAGCAGTTCTGTGGAGCAGCGGTGGCCGGCTAGG**ATG**
 GGCTGTCTCTGGGGTCTGGCTCTGCCCCTTTTCTTCTTCTGCTGGGAGGTTGGGGTCTCTGG
 GAGCTCTGCAGGCCCCAGCACCCGCGAGAGCAGACACTGCGATGACAACGGACGACACAGAAG
 TGCCCGCTATGACTCTAGCACCGGGCCACGCCGCTCTGGAAACTCAAACGCTGAGCGCTGAG
 ACCTCTTCTAGGGCCTCAACCCAGCCGGCCCCATTCCAGAAGCAGAGACCAGGGGAGCCAA
 GAGAATTTCCCCTGCAAGAGAGACCAGGAGTTTCACAAAAACATCTCCCAACTTCATGGTGC
 TGATCGCCACCTCCGTGGAGACATCAGCCGCCAGTGGCAGCCCCGAGGGAGCTGGAATGACC
 ACAGTTCAGACCATCACAGGCAGTGATCCCGAGGAAGCCATCTTTGACACCCTTTGCACCGA
 TGACAGCTCTGAAGAGGCAAAGACACTCACAATGGACATATTGACATTGGCTCACACCTCCA
 CAGAAGCTAAGGGCCTGTCTCAGAGAGCAGTGCCTCTTCCGACGGCCCCCATCCAGTCATC
 ACCCCGTCACGGGCCTCAGAGAGCAGCGCCTCTTCCGACGGCCCCCATCCAGTCATCACCCC
 GTCACGGGCCTCAGAGAGCAGCGCCTCTTCCGACGGCCCCCATCCAGTCATCACCCCCTCAT
 GGTCCCCGGGATCTGATGTCACTCTCCTCGCTGAAGCCCTGGTGACTGTCACAAACATCGAG
 GTTATTAATTGCAGCATCACAGAAATAGAAACAACAACTTCCAGCATCCCTGGGGCCTCAGA
 CATAGATCTCATCCCCACGGAAGGGGTGAAGGCCTCGTCCACCTCCGATCCACCAGCTCTGC
 CTGACTCCACTGAAGCAAAACCACACATCACTGAGGTACAGCCTCTGCCGAGACCCTGTCC
 ACAGCCGGCACACAGAGTCAGCTGCACCTCATGCCACGGTTGGGACCCCACTCCCCACTAA
 CAGCGCCACAGAAAGAGAAGTGACAGCACCCGGGGCCACGACCCTCAGTGGAGCTCTGGTCA
 CAGTTAGCAGGAATCCCCTGGAAGAAACCTCAGCCCTCTCTGTTGAGACACCAAGTTACGTC
 AAAGTCTCAGGAGCAGCTCCGGTCTCCATAGAGGCTGGGTCAGCAGTGGGCAAAACAACCTT
 CTTTGCTGGGAGCTCTGCTTCTCCTACAGCCCCCTCGGAAGCCGCCCTCAAGAACTTCACCC
 CTTTCAGAGACACCGACCATGGACATCGCAACCAAGGGGCCCTTCCCCACCAGCAGGGACCCT
 CTTCTTCTGTCCCTCCGACTACAACCAACAGCAGCCGAGGGACGAACAGCACCTTAGCCAA
 GATCACAACCTCAGCGAAGACCACGATGAAGCCCCAACAGCCACGCCACGACTGCCCCGGAC
 GAGGCCGACCACAGACG**TGA**GTGCAGGTGAAAATGGAGGTTTCCTCCTCCTGCGGCTGAGTG
 TGGCTTCCCCGGAAGACCTCACTGACCCCAGAGTGGCAGAAAGGCTGATGCAGCAGCTCCAC
 CGGGAACCTCACGCCACGCGCCTCACTTCCAGGTCTCCTTACTGCGTGTCAGGAGAGGCTA
 ACGGACATCAGCTGCAGCCAGGCATGTCCCGTATGCCAAAAGAGGGTGCTGCCCCTAGCCTG
 GGCCCCACCGACAGACTGCAGCTGCGTTACTGTGCTGAGAGGTACCCAGAAGGTTCCCATG
 AAGGGCAGCATGTCCAAGCCCCTAACCCCAGATGTGGCAACAGGACCCTCGCTCACATCCAC
 CGGAGTGTATGTATGGGGAGGGGCTTACCTGTTCCAGAGGTGTCCTTGGACTCACCTTGG
 CACATGTTCTGTGTTTCAGTAAAGAGAGACCTGATCACCCATCTGTGTGCTTCCATCCTGCA
 TTAAATTCACCTCAGTGTGGCCCCAAAAAAA

FIGURE 326

MGCLWGLALPLFFFCWEVGVSGSSAGPSTRRADTAMTTDDTEVPAMTLAPGHAALETQTL
 ETSSRASTPAGPIPEAETRGAKRISPARETRSFTKTSNFMVLIATSVETSAASGSPEGAGM
 TTVQTITGSDPEEAI FDTLCTDDSS EEA KTLTMDILT LAHTSTEAKGLSSESSASSD GPHPV
 ITPSRASESSASSD GPHPVITPSRASESSASSD GPHPVITPSWSPGSDVTLLAEALVTVTNI
 EVINCSITEIETTTSSIPGASDIDLIPTEGVKASSTSDPPALPDSTEAKPHITEVTASAETL
 STAGTTESAAPHATVGTPLPTNSATEREVTAPGATTLSGALVTVSRNPLEETSALSVETPSY
 VKVSGAAPVSIEAGSAVGKTTSFAGSSASSYSPSEAAALKNFTPSETPTMDIATKGPFPTSRD
 PLPSVPPTTTNSSRGTNSTLAKITTS AKTTMKPQQPRPRLPGRGRPQT

N-glycosylation sites:

amino acids 252-256, 445-449, 451-455

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 84-90

Casein kinase II phosphorylation sites.

amino acids 37-41, 108-112, 131-135, 133-137, 148-152, 165-169,
 246-250, 254-258, 256-260, 269-273, 283-287, 333-337, 335-339,
 404-408, 414-418, 431-435

N-myristoylation sites.

amino acids 2-8, 19-25, 117-123, 121-127, 232-238, 278-284, 314-
 320, 349-355, 386-392, 397-403, 449-455

ATP/GTP-binding site motif A (P-loop).

amino acids 385-393

FIGURE 327

GCGGAGCATCCGCTGCGGTCTCGCCGAGACCCCCGCGCGGATTGCGCCGGTCTTCCCGCGG
 GCGCGACAGAGCTGTCTCGCACCTGGATGGCAGCAGGGGCGCCGGGGTCTCTCGACGCCA
 GAGAGAAATCTCATCATCTGTGCAGCCTTCTTAAAGCAAACCTAAGACCAGAGGGAGGATTAT
 CCTTGACCTTTGAAGACCAAACTAACTGAAATTTAAAATGTTCTTCGGGGGAGAAGGGAG
 CTTGACTTACACTTTTGGTAATAATTTGCTTCCTGACACTAAGGCTGTCTGCTAGTCAGAATT
 GCCTCAAAAAGAGTCTAGAAGATGTTGTCATTGACATCCAGTCATCTCTTTCTAAGGGAATC
 AGAGGCAATGAGCCCGTATATACTTCAACTCAAGAAGACTGCATTAATTCTTGCTGTTCAAC
 AAAAAACATATCAGGGGACAAAGCATGTAACCTGATGATCTTCGACACTCGAAAAACAGCTA
 GACAACCCAACCTGCTACCTATTTTTCTGTCCCAACGAGGAAGCCTGTCCATTGAAACCAGCA
 AAAGGACTTATGAGTTACAGGATAATTACAGATTTTCCATCTTTGACCAGAAATTTGCCAAG
 CCAAGAGTTACCCCAGGAAGATTCTCTCTTACATGGCCAATTTTCACAAGCAGTCACTCCCC
 TAGCCCATCATCACACAGATTATTCAAAGCCCACCGATATCTCATGGAGAGACACACTTTCT
 CAGAAGTTTGGATCCTCAGATCACCTGGAGAACTATTTAAGATGGATGAAGCAAGTGCCCA
 GCTCCTTGCTTATAAGGAAAAAGGCCATTCTCAGAGTTCACAATTTTCTCTGATCAAGAAA
 TAGCTCATCTGCTGCCTGAAAATGTGAGTGCGCTCCAGCTACGGTGGCAGTTGCTTCTCCA
 CATAACACCTCGGCTACTCCAAAGCCCACCCTTCTACCCACCAATGCTTCAGTGACACC
 TTCTGGGACTTCCCAGCCACAGCTGGCCACCACAGCTCCACCTGTAACCACTGTCACTTCTC
 AGCCTCCCACGACCCTCATTTCTACAGTTTTTACACGGGCTGCGGCTACACTCCAAGCAATG
 GCTACAACAGCAGTTCTGACTACCACCTTTCAGGCACCTACGGACTCGAAAGGCAGCTTAGA
 AACCATAACGTTTACAGAAATCTCCAACCTTAACCTTTGAACACAGGGAATGTGTATAACCCTA
 CTGCACTTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAACTGCTTCCTGGGAAGGT
 AGGGAGGCCAGTCCAGGCAGTTCTCCAGGGCAGTGTTCCAGAAAATCAGTACGGCCTTCC
 ATTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGCTCTGTTCTCTGGTGATAGGCC
 TCGTCTCTCTGGGTAGAATCCTTTGGAATCACTCCGCAGGAAACGTTACTCAAGACTGGAT
 TATTTGATCAATGGGATCTATGTGGACATCTAAGGATGGAACCTCGGTGTCTCTTAATTCATT
 TAGTAACCAGAAGCCCAAATGCAATGAGTTTCTGCTGACTTGCTAGTCTTAGCAGGAGGTTG
 TATTTTGAAGACAGGAAAATGCCCCCTTCTGCTTTCCTTTTTTTTTTTGGAGACAGAGTCTT
 GCTCTGTTGCCAGGCTGGAGTGCAGTAGCACGATCTCGGCTCTCACCGCAACCTCCGTCTC
 CTGGGTTCAAGCGATTCTCCTGCCTCAGCCTCCTAAGTATCTGGGATTACAGGCATGTGCCA
 CCACACCTGGGTGATTTTTGTATTTTTAGTAGAGACGGGGTTTCACCATGTTGGTCAGGCTG
 GTCTCAAACCTCTGACCTAGTGATCCACCCTCCTCGGCCTCCCAAAGTGCTGGGATTACAGG
 CATGAGCCACCACAGCTGGCCCCCTTCTGTTTTATGTTTGGTTTTTGAAGAAGGAATGAAGTG
 GGAACCAAATTAGGTAATTTTGGGTAATCTGTCTCTAAAATATTAGCTAAAAACAAAGCTCT
 ATGTAAAGTAATAAAGTATAATTGCCATATAAATTTCAAATTCAACTGGCTTTTATGCAAA
 GAAACAGGTTAGGACATCTAGGTTCCAATTCATTACATTCTTGTTCCAGATAAAATCAAC
 TGTTTATATCAATTTCTAATGGATTTGCTTTTCTTTTATATGGATTCCTTTAAACTTATT
 CCAGATGTAGTTCCTTCCAATTAAATATTTGAATAAATCTTTTGTTACTCAA

FIGURE 328

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45410

><subunit 1 of 1, 431 aa, 1 stop

><MW: 46810, pI: 6.45, NX(S/T): 6

MFEGGEGSLTYTLVIICFLTLRLSASQNCLKKSLEDVVIDIQSSLKGIKRGNEPVYTSTQED
CINSCCSTKNISGDKACNLMIFDTRKTARQPCNYLFFCPNEEACPLKPAKGLMSYRIITDFP
SLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSDHLEKLF
KMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHHTSATPKPATLL
PTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATTAVLTTTFQAP
TDSKGSLETIPFTEISNLTNTGNVYNPTALSMSNVESSTMNKTASWEGREASPGSSSQGSV
PENQYGLPFEEKWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSLDYLINGIYVDI

Signal sequence.

amino acids 1-25

Transmembrane domain.

amino acids 384-405

N-glycosylation sites.

amino acids 72-76, 222-226, 251-255, 327-331, 352-356

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 415-419

Tyrosine kinase phosphorylation site.

amino acids 50-57

N-myristoylation sites.

amino acids 4-10, 48-54, 315-321

FIGURE 329

CTCCACGGTGTCCAGCGCCAGAAATGCGGCTTCTGGTCTGCTATGGGGTTGCCTGCTGCT
 CCCAGGTTATGAAGCCCTGGAGGGCCAGAGGAAATCAGCGGGTTCGAAGGGGACACTGTGT
 CCCTGCAGTGCACCTACAGGGAAGAGCTGAGGGACCACCGGAAGTACTGGTGCAGGAAGGGT
 GGGATCCTCTTCTCTCGCTGCTCTGGCACCATCTATGCAGAAGAAGAAGGCCAGGAGACAAT
 GAAGGGCAGGGTGTCCATCCGTGACAGCCGCCAGGAGCTCTCGCTCATTGTGACCCTGTGGA
 ACCTCACCCCTGCAAGACGCTGGGGAGTACTGGTGTGGGGTCGAAAAACGGGGCCCCGATGAG
 TCTTTACTGATCTCTCTGTTCTGTTTCCAGGACCCTGCTGTCTCCCTCCCCTTCTCCCAC
 CTTCCAGCCTCTGGCTACAACACGCCTGCAGCCCAAGGCAAAAGCTCAGCAAACCCAGCCCC
 CAGGATTGACTTCTCCTGGGCTCTACCCGGCAGCCACCACAGCCAAGCAGGGGAAGACAGGG
 GCTGAGGGCCCCCTCCATTGCCAGGGACTTCCCAGTACGGGCACGAAAGGACTTCTCAGTACAC
 AGGAACCTCTCCTCACCCAGCGACCTCTCCTCCTGCAGGGAGCTCCCCCCCCCCCCATGCAGC
 TGGACTCCACCTCAGCAGAGGACACCAGTCCAGCTCTCAGCAGTGGCAGCTCTAAGCCCAGG
 GTGTCCATCCCGATGGTCCGCATACTGGCCCCAGTCTGCTGGTGTGCTGAGCCTTCTGTGAGC
 CGCAGGCCTGATCGCCTTCTGCAGCCACCTGCTCCTGTGGAGAAAGGAAGCTCAACAGGCCA
 CGGAGACACAGAGGAACGAGAAGTTCTGGCTCTCACGCTTGAAGTGCAGGAGAAAAGGAAGCC
 CTTCCCAGGGCCCCCTGAGGGGGACGTGATCTCGATGCCTCCCCTCCACACATCTGAGGAGGA
 GCTGGGCTTCTCGAAGTTTGTCTCAGCGTAGGGCAGGAGGCCCTCCTGGCCAGGCCAGCAGT
 GAAGCAGTATGGCTGGCTGGATCAGCACCGATTCCCGAAAGCTTTCACCTCAGCCTCAGAG
 TCCAGCTGCCCCGACTCCAGGGCTCTCCCCACCCTCCCAGGCTCTCCTCTTGATGTTCCA
 GCCTGACCTAGAAGCGTTTGTGAGCCCTGGAGCCCAGAGCGGTGGCCTTGCTCTTCCGGCTG
 GAGACTGGGACATCCCTGATAGGTTACATCCCTGGGCAGAGTACCAGGCTGCTGACCCTCA
 GCAGGGCCAGACAAGGCTCAGTGGATCTGGTCTGAGTTTCAATCTGCCAGGAACCTCTGGGC
 CTCATGCCCAGTGTGCGACCCCTGCCTTCTCCTCCCACTCCAGACCCACCTTGTCTTCCCTCCC
 TGGCGTCTCAGACTTAGTCCCACGGTCTCCTGCATCAGCTGGTGTGATGAAGAGGAGCATGCT
 GGGGTGAGACTGGGATTCTGGCTTCTCTTTGAACCACCTGCATCCAGCCCTTCAGGAAGCCT
 GTGAAAAACGTGATTCTTGGCCCCACCAAGACCCACCAAAACCATCTCTGGGCTTGGTGCAG
 GACTCTGAATTCTAACAATGCCAGTGACTGTGCACTTGAGTTTGAGGGCCAGTGGGCCTG
 ATGAACGCTCACACCCCTTCAGCTTAGAGTCTGCATTTGGGCTGTGACGTCTCCACCTGCC
 CAATAGATCTGCTCTGTCTGCGACACCAGATCCACGTGGGGACTCCCCTGAGGCCTGCTAAG
 TCCAGGCCTTGGTCAGGTGAGGTGCACATTGCAGGATAAGCCCAGGACCGGCACAGAAGTGG
 TTGCCTTTNCCATTTGCCCTCCCTGGNCCATGCCTTCTTGCCTTTGGAAAAAATGATGAAGA
 AAACCTTGGCTCCTTCTTGTCTGGAAAGGGTTACTTGCCTATGGGTTCTGGTGGCTAGAGA
 GAAAAGTAGAAAACCAGAGTGCACGTAGGTGTCTAACACAGAGGAGAGTAGGAACAGGGCGG
 ATACCTGAAGGTGACTCCGAGTCCAGCCCCCTGGAGAAGGGGTGCGGGGTGGTGGTAAAGTA
 GCACAACTACTATTTTTTTTTCTTTTTCCATTATTATTGTTTTTTAAGACAGAATCTCGTGCT
 GCTGCCCAGGCTGGAGTGCAGTGGCACGATCTGCAAACCTCCGCCTCCTGGGTTCAAGTGATT
 CTTCTGCCTCAGCCTCCCGAGTAGCTGGGATTACAGGCACGCACCACCACACCTGGCTAATT
 TTTGTACTTTTAGTAGAGATGGGGTTTCACCATGTTGGCCAGGCTGGTCTTGAACCTCTGAC
 CTCAAATGAGCCTCCTGCTTCAGTCTCCCAAATTGCCGGGATTACAGGCATGAGCCACTGTG
 TCTGGCCCTATTTCTTTTAAAAAGTGAAATTAAGAGTTGTTTCTGATGCAAAACTTGGAAG
 ATGGAGGAGAAAAAGAAAAGGAAGAAAAAATGTCACCCATAGTCTCACCAGAGACTATCAT
 TATTTCTGTTTTGTTGTACTTCTTCCACTCTTTTCTTCTTACATAATTTGCCGGTGTCTT
 TTTACAGAGCAATTATCTTGTATATACTTTGTATCCTGCCTTTTCCACCTTATCGTTCC
 ATCACTTTATTCCAGCACTTCTCTGTGTTTTACAGACCTTTTTATAAATAAAATGTTTCATCA
 GCTGCATAAAAAAAAAAAAAA

FIGURE 330

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44196

<subunit 1 of 1, 332 aa, 1 stop

<MW: 36143, pI: 5.89, NX(S/T): 1

MRLLVLLWGCLLLPGYEALGPEEISGFEGDTVSLQCTYREELRDHRKYWCRKGGILFSRCS
GTIYAEEEGQETMKGRVSIRDSRQELSLIVTLWNLTLQDAGEYWCGVEKRGPDESLLISLFV
FPGPCCPPSPSPTFQPLATTRLQPKAKAQQTQPPGLTSPGLYPAATTAKQGKTGAEAPPLPG
TSQYGHERTSQYTGTSPHPATSPAGSSRPPMQLDSTSAEDTSPALSSGSSKPRVSIPMVRI
LAPVLVLLSLLSAAGLIAFCSHLLLWRKEAQQATETQRNEKFWLSRLTAAEEKEAPSQAPEGD
VISMPLHTSEEELGFSKFVSA

Important features:**Signal peptide:**

amino acids 1-17

Transmembrane domain:

amino acids 248-269

N-glycosylation site.

amino acids 96-99

Fibrinogen beta and gamma chains C-terminal domain.

amino acids 104-113

Ig like V-type domain:

amino acids 13-128